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OM protein - protein search, using sw model

Run on: August 9, 2001, 20:21:41 ; Search time 45.84 Seconds
(without alignments)
205.275 Million cell updates/sec

Title: US-09-367-013B-2
Perfect score: 2465
Sequence: 1 MAAPSVRTFTRAEVLNAEA.....EVSRLNEVSKASKMGKRAQ 457

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2465	100.0	457	2	US-08-834-655-2
2	2465	100.0	457	3	US-08-834-033A-2
3	2465	100.0	457	4	US-09-363-574-2
4	2465	99.6	457	2	US-08-833-610-4
5	2465	99.6	457	3	US-08-834-033A-14
6	1930	78.3	355	2	US-08-834-655-5
7	1930	78.3	355	3	US-08-834-033A-6
8	1930	78.3	355	4	US-09-363-574-5
9	514.5	20.9	446	2	US-08-833-610-5
10	514.5	20.9	446	3	US-08-834-033A-15
11	512.5	20.8	448	1	US-08-366-779-5
12	512.5	20.8	448	1	US-08-789-936-5
13	292.5	11.9	252	2	US-08-834-655-7
14	292.5	11.9	252	2	US-08-834-033A-8
15	292.5	11.9	252	4	US-09-363-574-7
16	284.5	11.5	446	2	US-08-833-610-2
17	284.5	11.5	446	3	US-08-834-033A-5
18	229	9.3	365	2	US-08-833-610-7
19	229	9.3	365	3	US-08-834-033A-17
20	210.5	8.5	359	1	US-08-307-382-2
21	210.5	8.5	359	1	US-08-366-779-2
22	210.5	8.5	359	1	US-08-478-727-2
23	210.5	8.5	359	1	US-08-473-508-2
24	210.5	8.5	359	1	US-08-789-936-2
25	210.5	8.5	359	2	US-08-833-610-6
26	210.5	8.5	359	3	US-08-834-033A-16
27	196.5	8.0	131	2	US-08-834-655-9

28	196.5	8.0	131	3	US-08-834-033A-10	Sequence 10, App1
29	196.5	8.0	131	4	US-09-363-574-9	Sequence 9, App1
30	184.5	7.5	143	3	US-08-834-655-11	Sequence 11, App1
31	184.5	7.5	143	3	US-08-834-033A-12	Sequence 12, App1
32	184.5	7.5	143	4	US-09-363-574-11	Sequence 11, App1
33	141	5.7	87	2	US-08-834-655-10	Sequence 10, App1
34	141	5.7	87	3	US-08-834-033A-11	Sequence 11, App1
35	141	5.7	87	4	US-09-363-574-10	Sequence 10, App1
36	136.5	5.5	186	2	US-08-833-610-3	Sequence 3, App1
37	136.5	5.5	186	3	US-08-834-033A-13	Sequence 13, App1
38	130.5	5.3	155	2	US-08-801-972-1	Sequence 1, App1
39	130.5	5.3	155	3	US-09-178-881-1	Sequence 8, App1
40	128.5	5.2	125	2	US-08-834-655-8	Sequence 8, App1
41	128.5	5.2	125	3	US-08-834-033A-9	Sequence 9, App1
42	128.5	5.2	125	4	US-09-363-574-8	Sequence 8, App1
43	127.5	5.2	382	2	US-08-811-177A-2	Sequence 2, App1
44	121	4.9	104	2	US-08-801-972-5	Sequence 5, App1
45	121	4.9	104	3	US-09-178-881-5	Sequence 5, App1

ALIGNMENTS

RESULT 1
US-08-834-655-2
; Sequence 2, Application US/08834655
; Patent No. 5968809
; GENERAL INFORMATION:
; APPLICANT: KNOTZER, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,655
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.124.00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400
; TELEFAX: (650) 328-4477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-834-655-2
Query Match 100.0%; Score 2465; DB 2; Length 457;
Best Local Similarity 100.0%; Pred. No. 1.8e-270;
Matches 457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAAPSVRTTAEVLAALNEGKKDAEAPFLMIIDNKVYDUREVPPHGGSVILTHV 60
1 MAAAPSVRTTAEVLAALNEGKKDAEAPFLMIIDNKVYDUREVPPHGGSVILTHV 60
Db 1 MAAAPSVRTTAEVLAALNEGKKDAEAPFLMIIDNKVYDUREVPPHGGSVILTHV 60
QY 61 GKDGTVDFTFHPBEAMETLANFYGDIDESDRIKNDPAAEVKRLRTLFOSLGYDSS 120
61 GKDGTVDFTFHPBEAMETLANFYGDIDESDRIKNDPAAEVKRLRTLFOSLGYDSS 120
Db 61 GKDGTVDFTFHPBEAMETLANFYGDIDESDRIKNDPAAEVKRLRTLFOSLGYDSS 120
QY 121 KAYYAFKVSFNLCTMGSLSTVYIAKMGQSTLANVLSAALLGLFMQCGMLAHDFLHOFV 180
121 KAYYAFKVSFNLCTMGSLSTVYIAKMGQSTLANVLSAALLGLFMQCGMLAHDFLHOFV 180
Db 121 KAYYAFKVSFNLCTMGSLSTVYIAKMGQSTLANVLSAALLGLFMQCGMLAHDFLHOFV 180
QY 181 ODRFWDLFGAFLGVCQGFSSSMWKDKNTHHAAPNVHGEDPDIDTHTLTMSEHALEM 240
181 ODRFWDLFGAFLGVCQGFSSSMWKDKNTHHAAPNVHGEDPDIDTHTLTMSEHALEM 240
Db 181 ODRFWDLFGAFLGVCQGFSSSMWKDKNTHHAAPNVHGEDPDIDTHTLTMSEHALEM 240
QY 241 FSDVDPDEELTRMSRPMVNLQTFEFPILSFARLSWCLOSILFVLPNGAHPGSGARVPI 300
241 FSDVDPDEELTRMSRPMVNLQTFEFPILSFARLSWCLOSILFVLPNGAHPGSGARVPI 300
Db 241 FSDVDPDEELTRMSRPMVNLQTFEFPILSFARLSWCLOSILFVLPNGAHPGSGARVPI 300
QY 301 SLVEQLSLAMHNTWYLATMFLFKDPVNMVLYFLVSOAVCGMLAIVFSLNHGMPIVSK 360
301 SLVEQLSLAMHNTWYLATMFLFKDPVNMVLYFLVSOAVCGMLAIVFSLNHGMPIVSK 360
Db 301 SLVEQLSLAMHNTWYLATMFLFKDPVNMVLYFLVSOAVCGMLAIVFSLNHGMPIVSK 360
QY 361 EBAVDMDEFTKQILITGRDVHPLGFANMFTGGLNYOLEHNLFPSPMRHNSKIOPAVETLC 420
361 EBAVDMDEFTKQILITGRDVHPLGFANMFTGGLNYOLEHNLFPSPMRHNSKIOPAVETLC 420
Db 361 EBAVDMDEFTKQILITGRDVHPLGFANMFTGGLNYOLEHNLFPSPMRHNSKIOPAVETLC 420
QY 421 KRYNRYHTTGMEIGTAEFVSRLENEVSKAASKMGKQ 457
421 KRYNRYHTTGMEIGTAEFVSRLENEVSKAASKMGKQ 457
Db 421 KRYNRYHTTGMEIGTAEFVSRLENEVSKAASKMGKQ 457

RESULT 2
US-08-834-033A-2
Sequence 2, Application US/08834033A
Patent No. 6075183
GENERAL INFORMATION:
APPLICANT: KUTZON, DEBORAH
APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834, 033A
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300, USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-033A-2

Query Match
Best Local Similarity 100.0%; Score 2465; DB 3; Length 457;
Matches 457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAAPSVRTTAEVLAALNEGKKDAEAPFLMIIDNKVYDUREVPPHGGSVILTHV 60
1 MAAAPSVRTTAEVLAALNEGKKDAEAPFLMIIDNKVYDUREVPPHGGSVILTHV 60
Db 1 MAAAPSVRTTAEVLAALNEGKKDAEAPFLMIIDNKVYDUREVPPHGGSVILTHV 60
QY 61 GKDGTVDFTFHPBEAMETLANFYGDIDESDRIKNDPAAEVKRLRTLFOSLGYDSS 120
61 GKDGTVDFTFHPBEAMETLANFYGDIDESDRIKNDPAAEVKRLRTLFOSLGYDSS 120
Db 61 GKDGTVDFTFHPBEAMETLANFYGDIDESDRIKNDPAAEVKRLRTLFOSLGYDSS 120
QY 121 KAYYAFKVSFNLCTMGSLSTVYIAKMGQSTLANVLSAALLGLFMQCGMLAHDFLHOFV 180
121 KAYYAFKVSFNLCTMGSLSTVYIAKMGQSTLANVLSAALLGLFMQCGMLAHDFLHOFV 180
Db 121 KAYYAFKVSFNLCTMGSLSTVYIAKMGQSTLANVLSAALLGLFMQCGMLAHDFLHOFV 180
QY 181 ODRFWDLFGAFLGVCQGFSSSMWKDKNTHHAAPNVHGEDPDIDTHTLTMSEHALEM 240
181 ODRFWDLFGAFLGVCQGFSSSMWKDKNTHHAAPNVHGEDPDIDTHTLTMSEHALEM 240
Db 181 ODRFWDLFGAFLGVCQGFSSSMWKDKNTHHAAPNVHGEDPDIDTHTLTMSEHALEM 240
QY 241 FSDVDPDEELTRMSRPMVNLQTFEFPILSFARLSWCLOSILFVLPNGAHPGSGARVPI 300
241 FSDVDPDEELTRMSRPMVNLQTFEFPILSFARLSWCLOSILFVLPNGAHPGSGARVPI 300
Db 241 FSDVDPDEELTRMSRPMVNLQTFEFPILSFARLSWCLOSILFVLPNGAHPGSGARVPI 300
QY 301 SLVEQLSLAMHNTWYLATMFLFKDPVNMVLYFLVSOAVCGMLAIVFSLNHGMPIVSK 360
301 SLVEQLSLAMHNTWYLATMFLFKDPVNMVLYFLVSOAVCGMLAIVFSLNHGMPIVSK 360
Db 301 SLVEQLSLAMHNTWYLATMFLFKDPVNMVLYFLVSOAVCGMLAIVFSLNHGMPIVSK 360
QY 361 EBAVDMDEFTKQILITGRDVHPLGFANMFTGGLNYOLEHNLFPSPMRHNSKIOPAVETLC 420
361 EBAVDMDEFTKQILITGRDVHPLGFANMFTGGLNYOLEHNLFPSPMRHNSKIOPAVETLC 420
Db 361 EBAVDMDEFTKQILITGRDVHPLGFANMFTGGLNYOLEHNLFPSPMRHNSKIOPAVETLC 420
QY 421 KRYNRYHTTGMEIGTAEFVSRLENEVSKAASKMGKQ 457
421 KRYNRYHTTGMEIGTAEFVSRLENEVSKAASKMGKQ 457
Db 421 KRYNRYHTTGMEIGTAEFVSRLENEVSKAASKMGKQ 457

RESULT 3
US-09-363-574-2
Sequence 2, Application US/09363574
Patent No. 6136574
GENERAL INFORMATION:
APPLICANT: KUTZON, DEBORAH
APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,574
FILING DATE:

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-202 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-363-574-2

Query Match 100.0%; Score 2465; DB 4; Length 457;
Best Local Similarity 100.0%; Pred. No. 1.8e-270;
Matches 457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPSVRTFTTAEVLNAEALNEGKDAEAPFLMIIDNKYVDREVPDPHGGSVILTHV 60
1 MAAPSVRTFTTAEVLNAEALNEGKDAEAPFLMIIDNKYVDREVPDPHGGSVILTHV 60
DB 61 GKGTGVDFDTHPEAEAMETLANFYVGDIDSDRDINKNDPAAEVRKRLTFLFOSLGYDSS 120
DB 61 GKGTGVDFDTHPEAEAMETLANFYVGDIDSDRDINKNDPAAEVRKRLTFLFOSLGYDSS 120
QY 121 KAYAEKVSFNLCIMGLSTYIVAKWGOTSTLANVLSAALLGLFMQCGWLHDFLHHQVF 180
121 KAYAEKVSFNLCIMGLSTYIVAKWGOTSTLANVLSAALLGLFMQCGWLHDFLHHQVF 180
DB 121 KAYAEKVSFNLCIMGLSTYIVAKWGOTSTLANVLSAALLGLFMQCGWLHDFLHHQVF 180
QY 181 QDRFWGDLFGAFLGVCQCGSSSMWKDKHNTHHAAPVHGEDPDIDTHPLTWSEHALEM 240
181 QDRFWGDLFGAFLGVCQCGSSSMWKDKHNTHHAAPVHGEDPDIDTHPLTWSEHALEM 240
DB 181 QDRFWGDLFGAFLGVCQCGSSSMWKDKHNTHHAAPVHGEDPDIDTHPLTWSEHALEM 240
QY 241 FSDVPDEELTRMSRFVNLQOTWFYFPLSFARLSWCLOSILFVLPFGAHRKSGARVP1 300
241 FSDVPDEELTRMSRFVNLQOTWFYFPLSFARLSWCLOSILFVLPFGAHRKSGARVP1 300
DB 241 FSDVPDEELTRMSRFVNLQOTWFYFPLSFARLSWCLOSILFVLPFGAHRKSGARVP1 300
QY 301 SLVEQLSLAMHWTYLATMFLFKDIPVNLVYFLVSAVGNLAIYFSLNHGMPYISK 360
301 SLVEQLSLAMHWTYLATMFLFKDIPVNLVYFLVSAVGNLAIYFSLNHGMPYISK 360
DB 301 SLVEQLSLAMHWTYLATMFLFKDIPVNLVYFLVSAVGNLAIYFSLNHGMPYISK 360
QY 361 EEAADMDFTKQIITGRDVRHGLFANMFTGGLNYQIEHHLFPPSMRHNFSKIQPAVETLC 420
361 EEAADMDFTKQIITGRDVRHGLFANMFTGGLNYQIEHHLFPPSMRHNFSKIQPAVETLC 420
DB 361 EEAADMDFTKQIITGRDVRHGLFANMFTGGLNYQIEHHLFPPSMRHNFSKIQPAVETLC 420
QY 421 KKNVRYHTTGMTEGTAEVFSRLNEVSKASKMGKAQ 457
421 KKNVRYHTTGMTEGTAEVFSRLNEVSKASKMGKAQ 457
DB 421 KKNVRYHTTGMTEGTAEVFSRLNEVSKASKMGKAQ 457

RESULT 4
US-08-833-610-4

Sequence 4, Application US/08833610
Patent No. 5972664
GENERAL INFORMATION:
APPLICANT: KNOTZON, DEBORAH
APPLICANT: MURKERTJ, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SONITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVE, P.O. BOX 60039
CITY: PALO ALTO

STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,610
FILING DATE: 11-Apr-1997

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.123.000S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)328-4400
TELEFAX: (650)328-4477
TELEX: N/A

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-833-610-4

Query Match 99.6%; Score 2456; DB 2; Length 457;
Best Local Similarity 99.8%; Pred. No. 1.9e-269;
Matches 456; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAPSVRTFTTAEVLNAEALNEGKDAEAPFLMIIDNKYVDREVPDPHGGSVILTHV 60
1 MAAPSVRTFTTAEVLNAEALNEGKDAEAPFLMIIDNKYVDREVPDPHGGSVILTHV 60
DB 61 GKGTGVDFDTHPEAEAMETLANFYVGDIDSDRDINKNDPAAEVRKRLTFLFOSLGYDSS 120
61 GKGTGVDFDTHPEAEAMETLANFYVGDIDSDRDINKNDPAAEVRKRLTFLFOSLGYDSS 120
DB 61 GKGTGVDFDTHPEAEAMETLANFYVGDIDSDRDINKNDPAAEVRKRLTFLFOSLGYDSS 120
QY 121 KAYAEKVSFNLCIMGLSTYIVAKWGOTSTLANVLSAALLGLFMQCGWLHDFLHHQVF 180
121 KAYAEKVSFNLCIMGLSTYIVAKWGOTSTLANVLSAALLGLFMQCGWLHDFLHHQVF 180
DB 121 KAYAEKVSFNLCIMGLSTYIVAKWGOTSTLANVLSAALLGLFMQCGWLHDFLHHQVF 180
QY 181 QDRFWGDLFGAFLGVCQCGSSSMWKDKHNTHHAAPVHGEDPDIDTHPLTWSEHALEM 240
181 QDRFWGDLFGAFLGVCQCGSSSMWKDKHNTHHAAPVHGEDPDIDTHPLTWSEHALEM 240
DB 181 QDRFWGDLFGAFLGVCQCGSSSMWKDKHNTHHAAPVHGEDPDIDTHPLTWSEHALEM 240
QY 241 FSDVPDEELTRMSRFVNLQOTWFYFPLSFARLSWCLOSILFVLPFGAHRKSGARVP1 300
241 FSDVPDEELTRMSRFVNLQOTWFYFPLSFARLSWCLOSILFVLPFGAHRKSGARVP1 300
DB 241 FSDVPDEELTRMSRFVNLQOTWFYFPLSFARLSWCLOSILFVLPFGAHRKSGARVP1 300
QY 301 SLVEQLSLAMHWTYLATMFLFKDIPVNLVYFLVSAVGNLAIYFSLNHGMPYISK 360
301 SLVEQLSLAMHWTYLATMFLFKDIPVNLVYFLVSAVGNLAIYFSLNHGMPYISK 360
DB 301 SLVEQLSLAMHWTYLATMFLFKDIPVNLVYFLVSAVGNLAIYFSLNHGMPYISK 360
QY 361 EEAADMDFTKQIITGRDVRHGLFANMFTGGLNYQIEHHLFPPSMRHNFSKIQPAVETLC 420
361 EEAADMDFTKQIITGRDVRHGLFANMFTGGLNYQIEHHLFPPSMRHNFSKIQPAVETLC 420
DB 361 EEAADMDFTKQIITGRDVRHGLFANMFTGGLNYQIEHHLFPPSMRHNFSKIQPAVETLC 420
QY 421 KKNVRYHTTGMTEGTAEVFSRLNEVSKASKMGKAQ 457
421 KKNVRYHTTGMTEGTAEVFSRLNEVSKASKMGKAQ 457
DB 421 KKNVRYHTTGMTEGTAEVFSRLNEVSKASKMGKAQ 457

RESULT 5
US-08-834-033A-14

Sequence 14, Application US/08834033A
Patent No. 6075183
GENERAL INFORMATION:
APPLICANT: KNOTZON, DEBORAH

Db 241 LLAIVFSLNHNMGMPVISEEAVDMDFETKQIITGRDHPGLFANWFGGLVYQIEHHLFP 300
QY 403 SMPRHNSKIOPAVEITLCKKYNVRYHTTGMEGTAEVFSRLNEVSKAASKMGKAO 457
Db 301 SMPRHNSKIOPAVEITLCKKYNVRYHTTGMEGTAEVFSRLNEVSKAASKMGKAO 355

RESULT 7

US-08-834-033A-6

; Sequence 6, Application US/08834033A

; Patent No. 6075183

; GENERAL INFORMATION:

; APPLICANT: KNOTZON, DEBORAH

; APPLICANT: MUKERJI, PRADIP

; APPLICANT: HUANG, YUNG-SHENG

; APPLICANT: THUDMOND, JENNIFER

; APPLICANT: CHAUDHARY, SUNITA

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.

; STREET: 2001 FERRY BUILDING

; CITY: SAN FRANCISCO

; STATE: CA

; COUNTRY: USA

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:

; FILING DATE: 11-Apr-1997

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: WARD, MICHAEL R.

; REGISTRATION NUMBER: 38,651

; REFERENCE/DOCKET NUMBER: CGAB-300.USA

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 433-4150

; TELEFAX: (415) 433-8716

; TELEX: N/A

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 355 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-834-033A-6

Query Match 78.3%; Score: 1930; DB 3; Length 355;
Best Local Similarity 100.0%; Pred. No. 4.8e-210;

Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 EVKRLRTLFOSLGYDSSKATYARVSNLCIMGISTYIVAKWGOTSTLANVLSAALLGL 162
Db 1 EVKRLRTLFOSLGYDSSKATYARVSNLCIMGISTYIVAKWGOTSTLANVLSAALLGL 60

QY 163 FMOQCGMLAHDFLHNOVFQDRFWDGLFGAFLGVCQCGFSSMMWKDKNTHHAAPVHGED 222
Db 61 FMOQCGMLAHDFLHNOVFQDRFWDGLFGAFLGVCQCGFSSMMWKDKNTHHAAPVHGED 120

QY 223 PDIDTHPLLTWSEHALEMFSDVPDEELTRMWSRPMVNLQOTWFYFPIISFARLSMCLOSIL 282
Db 121 PDIDTHPLLTWSEHALEMFSDVPDEELTRMWSRPMVNLQOTWFYFPIISFARLSMCLOSIL 180

QY 283 FVLENGAHKFSGARVPISLVEQLSLAMHWTWYATNMFLETKDPVNMVLYFVSQAVCGN 342
Db 121 PDIDTHPLLTWSEHALEMFSDVPDEELTRMWSRPMVNLQOTWFYFPIISFARLSMCLOSIL 180

Db 181 FVLENGAHKFSGARVPISLVEQLSLAMHWTWYATNMFLETKDPVNMVLYFVSQAVCGN 240

QY 343 LLAIVFSLNHNMGMPVISEEAVDMDFETKQIITGRDHPGLFANWFGGLVYQIEHHLFP 402
Db 241 LLAIVFSLNHNMGMPVISEEAVDMDFETKQIITGRDHPGLFANWFGGLVYQIEHHLFP 300

QY 403 SMPRHNSKIOPAVEITLCKKYNVRYHTTGMEGTAEVFSRLNEVSKAASKMGKAO 457
Db 301 SMPRHNSKIOPAVEITLCKKYNVRYHTTGMEGTAEVFSRLNEVSKAASKMGKAO 355

RESULT 8

US-09-363-574-5

; Sequence 5, Application US/09363574

; Patent No. 6136574

; GENERAL INFORMATION:

; APPLICANT: KNOTZON, DEBORAH

; APPLICANT: MUKERJI, PRADIP

; APPLICANT: HUANG, YUNG-SHENG

; APPLICANT: THUDMOND, JENNIFER

; APPLICANT: CHAUDHARY, SUNITA

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.

; STREET: 2001 FERRY BUILDING

; CITY: SAN FRANCISCO

; STATE: CA

; COUNTRY: USA

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; FILING DATE: 09/09/363,574

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: WARD, MICHAEL R.

; REGISTRATION NUMBER: 38,651

; REFERENCE/DOCKET NUMBER: CGAB-202 USA

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 433-4150

; TELEFAX: (415) 433-8716

; TELEX: N/A

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 355 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-09-363-574-5

Query Match 78.3%; Score: 1930; DB 4; Length 355;
Best Local Similarity 100.0%; Pred. No. 4.8e-210;

Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 EVKRLRTLFOSLGYDSSKATYARVSNLCIMGISTYIVAKWGOTSTLANVLSAALLGL 162
Db 1 EVKRLRTLFOSLGYDSSKATYARVSNLCIMGISTYIVAKWGOTSTLANVLSAALLGL 60

QY 163 FMOQCGMLAHDFLHNOVFQDRFWDGLFGAFLGVCQCGFSSMMWKDKNTHHAAPVHGED 222
Db 61 FMOQCGMLAHDFLHNOVFQDRFWDGLFGAFLGVCQCGFSSMMWKDKNTHHAAPVHGED 120

QY 223 PDIDTHPLLTWSEHALEMFSDVPDEELTRMWSRPMVNLQOTWFYFPIISFARLSMCLOSIL 282
Db 121 PDIDTHPLLTWSEHALEMFSDVPDEELTRMWSRPMVNLQOTWFYFPIISFARLSMCLOSIL 180

QY 283 FVLENGAHKFSGARVPISLVEQLSLAMHWTWYATNMFLETKDPVNMVLYFVSQAVCGN 342
Db 121 PDIDTHPLLTWSEHALEMFSDVPDEELTRMWSRPMVNLQOTWFYFPIISFARLSMCLOSIL 180

0Y	283	FVLPBGQAHKRSKGARVRLSTLYEOLSLAMHHMHWLTATMFLFKDPDVNMLYYELVLSQAACGN	34.2
Db	181	FVLPRGQAHKRSKGARVRLSTLYEOLSLAMHHMHWLTATMFLFKDPDVNMLYYELVLSQAACGN	24.0
0Y	343	LLATVFSLNHHGMVVISKEEAVNDPFTKQITIGRDVPHGLFAMWFTGSLNYOLEHHLP	40.2
Db	241	LLATVFSLNHHGMVVISKEEAVNDPFTKQITIGRDVPHGLFAMWFTGSLNYOLEHHLP	30.0
0Y	403	SMPRHNEKIDPAVETLCKKRVNRYHTTGMIEGFAEYFSRLNEVSKAASKMGAAQ	45.7
Db	301	SMPRHNEKIDPAVETLCKKRVNRYHTTGMIEGFAEYFSRLNEVSKAASKMGAAQ	35.5

RESULT

```

US-08-833-610-5
Sequence 5, Application US/08833610
Patent No. 5972664
GENERAL INFORMATION:
APPLICANT: KNOTZON, DEBORAH
APPLICANT: MURKERT, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: RAE-VENTNER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,610
FILING DATE: 11 APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTNER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.123.000S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)328-4400
TELEFAX: (650)328-4477
TELNET: N/A
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-833-610-5

```

Query Match	20.98;	Score 514.5;	DB 2;	Length 446;
Best Local Similarity	32.28;	Pred. No. 1.5e-49;		
Matches 136;	Conservative 62;	Mismatches 183;	Indels 41;	Gaps 14

[illegible]

Oy	149	STLNVLSAALLGFTMOCCGLADFLHNOYFORFEGDLEFGALGCVCGFSSSWKDK	208
Db	136	GVVLHLEFGCGCLMGFLMQSGVIGHDAGHYVSDSRINKTKMGIFAAACLSGISIGMKMN	195
Oy	209	HNTHHAPNVHGEDPDIDHPLTWSEHAL-EMFSDVPDEELT-RKMSRPMVNLQWTFYF	266
Db	196	HNHHHICNLSLEYRDPDQIYFPLVSSKEFGSLSHYFKRLTDSLSRFVSYOHNTFY	255
Oy	267	PILSFARLSCLOSILFVLPYRGOAHKFGSARVPLISLEOGLSLMHNYLATWFLFKDP	326
Db	256	PIMCARLNMVYQSLIML-----TKRNVSYRAEELIGCLVFSIMY-PLVSLCPNM	306
Oy	327	VNMLVYFVSQAVCGNLLAIYFSLNHNQMPY-ISKBAVDMDFFTKQIITGRDYNBFLA	385
Db	307	GERIMFVYASLSVYG-MQOYQFSLNTHSSSYUYGKPRG--NNMEKOTDGLDISCPMM	363
Oy	386	NMFTGGLNLYQLEIHNLFPSMRPHNSKLTQPAVELTJCKRYNVRNHTGMIESTAEVFSRLNE	445
Db	364	DMFHGGIGLOFQIENHLPFRMPRCNLRKISIPYUETJELCKKHNLRYNVAS-----FSKANE	415
Oy	446	VS 447	
Db	416	MT 417	

RESULT 10

US-08-834-033A-15
Sequence 15, Application US/08834033A
Patent No. 6075183

GENERAL INFORMATION:

APPLICANT: KNOTZON, DEBORAH
APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,033A
FILING DATE: 11-Apr-1997

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300, USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-834-033A-15

Query Match 20.9%; Score 514.5; DB 3; Length 446;

Best Local Similarity 32.2%; Pred. No. 1.5e+49; Indels 41; Gaps 14;
 Matches 136; Conservative 62; Mismatches 183;

36 IDKKYDVEEFVDPHGGSVILTHV-GKDTVDFFPHPEAAMETLANFYVGDIDSDRD 94
 27 ICKKAVDSDWVDHGGSPFLKSLAGQEVTDAFVAFHNPASTWKNLKDFFTG---YLLKD 83

95 IKNDFAEAEYRKRLTLPFOSIGYDSSKAYAF-----KVSFNLCTIGLSTVIYAKGQT 148
 84 YSVSEVSKDYRKLVFEFSKMGLYD-KKGHIMFATLCEFIAMLFAMSYG---VLECE---- 135

149 STLANTLSAALLGLFMQOCGMLANHDLHNOYFODREFWGLFGAFLGVCOGFSSMMKDK 208
 136 GVLVHLFSGCLMGFLMIQSGWIGHDAGHYVSDSLNKFMGIFANCLSGISIGMKWN 195

209 HNTNHAAPNVGEBDPDIDTHPLLTWSEHAL-EMFSDVPDELT-RMWSRPMVLNQTWYF 266
 196 HNHHTACNSLEVDPLDQYIPFLVSSKFFGSLTSHFEKRLTFDSLRFFVSYQHTFY 255

267 PILSFARLSMCLQSLFVLPNGAHKPSGARVPISLVEQLSLAMHNTWYLATMFLPKDP 336
 256 PIMCARLNNYVQSLIMLT-----TKRNVSYRAOELLGCLVFSIMY-PLLVSCLPNW 306

327 VNNLVYFLVSAQCNLALVFSLNHNGMPY-ISKEADVMDPFTKOITGRDVHPGLFA 385
 307 GERIMFVLASLVYG-MQOVQFSLNHFSSSYVYKPKG--NNMFEKOTDGLDISCPWM 363

386 NMFTGGLNIOIEHNLFPSPMRHNSKIOPAVETLCKKYNRYHTGTGIECTAEVFSRLNE 445
 364 DMFHGSGQFOIEHNLFPKMRCLRKISPYIELCKKHNLPLYNAS-----FSKANE 415

446 VS 447
 416 MT 417

RESULT 11
 US-08-366-779-5
 ; Sequence 5, Application US/08366779
 ; Patent No. 5614393
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; APPLICANT: Reddy, Avutu S.
 ; APPLICANT: Nuccio, Michael
 ; APPLICANT: Freysinet, Georges L.
 ; APPLICANT: Nunberg, Andrew N.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/366,779
 ; FILING DATE: 30-DEC-1994
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Presser, Leopold
 ; REGISTRATION NUMBER: 19,827
 ; REFERENCE/DOCKET NUMBER: 8383ZYXW
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 448 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 US-08-366-779-5

Query Match 20.8%; Score 512.5; DB 1; Length 448;
 Best Local Similarity 32.0%; Pred. No. 2.6e+49;
 Matches 135; Conservative 63; Mismatches 183; Indels 41; Gaps 14;

36 IDKKYDVEEFVDPHGGSVILTHV-GKDTVDFFPHPEAAMETLANFYVGDIDSDRD 94
 27 ICKKAVDSDWVDHGGSPFLKSLAGQEVTDAFVAFHNPASTWKNLKDFFTG---YLLKD 83

95 IKNDFAEAEYRKRLTLPFOSIGYDSSKAYAF-----KVSFNLCTIGLSTVIYAKGQT 148
 84 YSVSEVSKDYRKLVFEFSKMGLYD-KKGHIMFATLCEFIAMLFAMSYG---VLECE---- 135

149 STLANTLSAALLGLFMQOCGMLANHDLHNOYFODREFWGLFGAFLGVCOGFSSMMKDK 208
 136 GVLVHLFSGCLMGFLMIQSGWIGHDAGHYVSDSLNKFMGIFANCLSGISIGMKWN 195

209 HNTNHAAPNVGEBDPDIDTHPLLTWSEHAL-EMFSDVPDELT-RMWSRPMVLNQTWYF 266
 196 HNHHTACNSLEVDPLDQYIPFLVSSKFFGSLTSHFEKRLTFDSLRFFVSYQHTFY 255

267 PILSFARLSMCLQSLFVLPNGAHKPSGARVPISLVEQLSLAMHNTWYLATMFLPKDP 336
 256 PIMCARLNNYVQSLIMLT-----TKRNVSYRAOELLGCLVFSIMY-PLLVSCLPNW 306

327 VNNLVYFLVSAQCNLALVFSLNHNGMPY-ISKEADVMDPFTKOITGRDVHPGLFA 385
 307 GERIMFVLASLVYG-MQOVQFSLNHFSSSYVYKPKG--NNMFEKOTDGLDISCPWM 363

386 NMFTGGLNIOIEHNLFPSPMRHNSKIOPAVETLCKKYNRYHTGTGIECTAEVFSRLNE 445
 364 DMFHGSGQFOIEHNLFPKMRCLRKISPYIELCKKHNLPLYNAS-----FSKANE 415

446 VS 447
 416 MT 417

RESULT 12
 US-08-789-936-5
 ; Sequence 5, Application US/08789936
 ; Patent No. 5789220
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; APPLICANT: Reddy, Avutu S.
 ; APPLICANT: Nuccio, Michael
 ; APPLICANT: Freysinet, Georges L.
 ; APPLICANT: Nunberg, Andrew N.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/789,936

CORRESPONDENCE ADDRESS:

ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 9, 2001, 20:20:06 ; Search time 79.24 Seconds
(without alignments)
349.636 Million cell updates/sec

Title: US-09-367-013B-2

Perfect score: 2465

Sequence: 1 MAAPSVRTETRAEVLENAEA.....EVPRLNEVSKAKMGKQAQ 457

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2465	100.0	457	19	AAW84137
2	2465	100.0	457	20	AAW95504
3	2465	100.0	457	21	AAV92599
4	2465	100.0	457	21	AAV56045
5	2465	100.0	457	22	AAW831684
6	2465	99.6	457	20	AAW85121
7	1930	78.3	355	19	AAW84139
8	873	35.4	520	22	AAW846440
9	841.5	34.1	483	22	AAW846435
10	841.5	34.1	483	22	AAW846436
11	818	33.2	525	21	AAV51354

12	818	33.2	525	22	AAW846810
13	631	25.6	422	21	AAV96722
14	629	25.5	447	20	AAV21891
15	629	25.5	447	21	AAV96721
16	615.5	25.0	454	21	AAV51355
17	557	22.6	443	20	AAV17751
18	549	22.3	448	21	AAV71551
19	537	21.8	473	21	AAV51353
20	534.5	21.7	458	21	AAV51348
21	524.5	21.3	444	21	AAV95445
22	524.5	21.3	444	22	AAW831686
23	523.5	21.2	444	21	AAV97538
24	523	21.2	462	21	AAV71552
25	522	21.2	449	21	AAW53861
26	522	21.2	449	21	AAV51334
27	521	21.1	449	21	AAW07392
28	521	21.1	517	21	AAW07391
29	518.5	21.0	448	17	AAW98455
30	518.5	21.0	448	19	AAW67471
31	518.5	21.0	448	20	AAW98130
32	515.5	20.9	448	21	AAV51349
33	514.5	20.9	446	20	AAW85122
34	508.5	20.6	444	21	AAW41898
35	502.5	20.4	450	21	AAV71554
36	502	20.4	449	21	AAV51333
37	497.5	20.2	449	21	AAW29290
38	493	20.0	469	21	AAV71555
39	478.5	19.4	432	21	AAV95446
40	478.5	19.4	445	21	AAV97540
41	478.5	19.4	445	21	AAV83229
42	478.5	19.4	746	19	AAW84156
43	478.5	19.4	746	20	AAW85135
44	478.5	19.4	752	21	AAV92618
45	478.5	19.4	753	20	AAV95514

ALIGNMENTS

RESULT 1	
AAW84137	
ID AAW84137 standard; Protein; 457 AA.	
AC	
XX AAW84137;	
DT 15-FEB-1999 (first entry)	
XX	
XX	
DE A delta-6 desaturase enzyme.	
XX	
KW Fatty acid: delta-6 desaturase; polyunsaturated fatty acid;	
KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;	
KW cancer; diabetes; eczema; platelet aggregation; vasodilation;	
KW cholesterol level; endometriosis; premenstrual syndrome;	
KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;	
KW acute respiratory syndrome; hypertension; inflammatory skin disorder.	
XX	
OS Mortierella alpina.	
XX	
PN WO9846763-A1.	
PD 22-OCT-1998.	
XX	
PF 10-APR-1998; 98MO-US07126.	
XX	
PR 11-APR-1997; 97US-0834655.	
XX	
PA (ABBO) ABBOTT LAB.	
PA (CALD) CALGENE LLC.	
XX	
PI Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P;	
PI Thurnmond J;	
XX	
DR WPI; 1998-594582/50.	

P. patens delta6-d
E. gracilis fatty
C. elegans delta 5
C. elegans fatty a
Protein 25bce with
Caenorhabditis ele
Florida bitterbush
protein b5cae with
Sphingolipid desat
Human delta-5-desat
Amino acid sequenc
Human fatty acid d
Corn sphingolipid
Arabidopsis thalia
A. thaliana sldi p
Arabidopsis thalia
Arabidopsis thalia
Borage delta-6-des
Borage delta-6-des
Sunflower HADES pr
A delta-6 desatura
Human ORF ORF1762
Soybean sphingolip
B. napus sldi prot
Arabidopsis thalia
Wheat sphingolipid
Human delta-5-desat
Human fatty acid d
CyB5RP fatty acid
Human desaturase e
A desaturase enzym
Human desaturase h
Amino acid sequenc

DR N-PSDB; AAV63624.
XX New isolated fatty acid desaturase enzymes - used for the production
PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical
XX compositions, nutritional compositions, cosmetics or animal feed
XX
PS Claim 3; Fig 3A-E; 165pp; English.
XX
CC The present sequence represents a Mortierella alpina fatty acid delta-6
CC desaturase enzyme. The enzyme sequence is used in the methods of
CC the invention. The specification describes methods for desaturating a
CC fatty acid and for producing a desaturated fatty acid by expressing
CC increased levels of a desaturase. The present desaturase is an enzyme
CC which introduces a double bond carbons 6 and 7 from the carboxyl end of
CC a fatty acid molecule. The enzyme can be used for desaturating fatty
CC acids. The enzyme can be used to produce polyunsaturated fatty acids,
CC which can be used for treating malnutrition, in pharmaceutical
CC compositions, in cosmetics or in animal feed. The polyunsaturated fatty
CC acids can be used for treating e.g. restenosis after angioplasty,
CC inflammation, rheumatoid arthritis, asthma, psoriasis, cancer, diabetes
CC or eczema or reduce blood pressure. They can also be used to inhibit
CC platelet aggregation, cause vasodilation, lower cholesterol levels,
CC inhibit proliferation of vessel wall smooth muscle and fibrous tissue,
CC reduce or prevent gastro-intestinal bleeding and other side effects
CC caused by non-steroidal anti-inflammatory drugs, prevent or treat
CC endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis
CC and chronic fatigue after viral infections, treat AIDS, multiple
CC sclerosis, acute respiratory syndrome, hypertension and inflammatory skin
CC disorders.
XX
XX Sequence 457 AA:
S0
Query Match 100.0%; Score 2465; DB 19; Length 457;
Best Local Similarity 100.0%; Pred. No. 1.1e-245;
Matches 457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAPSVRTFTFAEVLNENALNEGRKDAEAPLMTIDNKVYVREVPDHPGCVLTFFH 60
DB 1 maapsvrtftfraevlnenalnegrkdaepflmtidnkvyvrefvphpgsvlthtv 60
QY 61 GKGDTVDTEHPEAAMETLANFVGDIDESDRDKNDFAEVRKRLTFLQSLGYDSS 120
DB 61 gkgdvtvdtehp eaametlanfv gdid esdrdkndfae vrkrlt flqslgydss 120
QY 61 gkgdvtvdtehp eaametlanfv gdid esdrdkndfae vrkrlt flqslgydss 120
DB 61 gkgdvtvdtehp eaametlanfv gdid esdrdkndfae vrkrlt flqslgydss 120
QY 121 KAYAFKVSFNLCTGLSTVYAKWGQSTLANVLSAALLGFMQCCGLANDFLHQYF 180
DB 121 kayafkvsfnlctglstvyakwgqstlanvlsaal lglfmqccgl andflhqyf 180
QY 181 QDRFWDGDFGAFILGVCQGFSSSMWKDKNTHNAPNVHGEPPDIDTFLPLTWSHLELM 240
DB 181 qdrfwdgdfgafilgvcqgfsssmwkdknthnapnv hgeppdidtflpl twshelem 240
QY 241 FSDVDEELTRMSRFVNLQNTWEYFPLISFARLSWCLQSLIFVLNPGQAHKPSGARVPI 300
DB 241 fsdvdeelt rmsrfvnlqntwey fplisfarlsw clqslifvlnpgqahkpsgarvpi 300
QY 241 fsdvdeelt rmsrfvnlqntwey fplisfarlsw clqslifvlnpgqahkpsgarvpi 300
DB 241 fsdvdeelt rmsrfvnlqntwey fplisfarlsw clqslifvlnpgqahkpsgarvpi 300
QY 301 SLVEGLSLAMHTWTLATMFLFIKRPVMMLYFLVSAQVCGMLAIVSLNHNKRPVISK 360
DB 301 slveglslamhtw tlatmflfikrpvmmlyflvsa qvcm laivsln hnkprv isk 360
QY 361 BEAVMDPFTKOIITGRVHNGELFANWFTGGLNVOIEHHLRPSMRHNSKTOPAVETLC 420
DB 361 beavmdpftkoiit grvhngelfanwftggl nvoie hhlrpsmr hnskto pavetlc 420
QY 421 KKYNVRYHTTGIECTAEVSRLENSVSKASRMKRAQ 457
DB 421 kkyvryhttgie ctavsrle nsvskasrmkra q 457
RESULT 2
AAW95504
ID: AAW95504 standard; peptide: 457 AA.

XX AAW95504;
AC 26-MAR-1999 (first entry)
XX
DE Mortierella alpina delta 6 desaturase.
XX
KM Delta 6 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil;
KM polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;
KM stearidonic acid; eicosapentaenoic acid; main nutrition; feeding formula;
KM dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;
KM rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;
KM diabetes; cosmetic; animal feed.
XX
OS Mortierella alpina.
XX
PN W09846764-A1.
XX
XX 22-OCT-1998.
XX
PD 10-APR-1998; 98WO-US07421.
XX
PF 24-OCT-1997; 97US-0956985.
XX
PR 11-APR-1997; 97US-0833610.
XX
PR 11-APR-1997; 97US-0834033.
XX
XX 11-APR-1997; 97US-0834655.
XX
PA (ABBO) ABBOTT LAB.
PA (CALJ) CALGENE LLC.
XX
XX Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P;
XX Thurmond J;
XX WPI, 1999-080739/07.
XX N-PSDB; AAX00889.
XX
PT Nucleic acid construct able to express fatty acid desaturase in
PT plants - useful in human or animal nutrition, as cosmetics and
PT therapeutically, e.g. for restenosis, cancer and diabetes
XX
PS Claim 7; Fig 3A-E; 210pp; English.
XX
XX This represents a Mortierella alpina delta 6 desaturase. The invention
XX relates to a nucleic acid construct that contains at least one of the
XX nucleotide sequences (AAX00889 to AAX00891) encoding M. alpina delta 6,
XX delta 12 and delta 5 desaturases (AAW95504 to AAW95506) respectively,
XX coupled to an expression control sequence functional in plants.
XX Recombinant plant cells containing at least one DNA encoding a M. alpina
XX fatty acid desaturase (FAD), can be used for the production of
XX polyunsaturated fatty acid (PUFA). These recombinant cells or plants
XX containing them are used to produce oils such as linoleic acid
XX arachidonic acid, gamma-linolenic acid, dihomo-gamma-linolenic acid,
XX stearidonic acid and eicosapentaenoic acid (EPA). These plant oils are
XX used: (i) to treat malnutrition; (ii) in infant feeding formulas, or
XX dietary supplements or substitutes, for use in humans or animals; (iii)
XX for treating disorders associated with inadequate consumption or
XX production of PUFA (or their metabolites such as prostaglandins), e.g.
XX restenosis after angioplasty, inflammation, AIDS, Rheumatoid arthritis,
XX psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics, and
XX (v) as animal feeds. Fragments of the DNA are used as probes to isolate
XX related coding sequences. Recombinant plants can produce high yields of
XX PUFA, since new pathways can be created and unwanted ones suppressed.
XX Plants can be engineered to express oils of particular PUFA composition,
XX e.g. one similar to that in human milk, and product recovery is simpler
XX than with e.g. fish.
XX
S0 Sequence 457 AA:
Query Match 100.0%; Score 2465; DB 20; Length 457;
Best Local Similarity 100.0%; Pred. No. 1.1e-245;
Matches 457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAAPSVRTFRAVLVAALNECKXAEAPLMIIDNKYDVREYDPHGGSVLITTH	60
Db	1	maapsvrtfrraevlaaealneqkkaaeapfmiidnkdydvretvdpdpgssvlltth	60
QY	61	GKDGTVDFEFTFHPREAAEETIANFVGDIDESSDRDINKDDPAEAYRKIRLTFOSLGYDSS	120
Db	61	gkdgdvdftrfhpaaaeetianfyvgdidessdrdknddfaeayrklrtltfsglyyds	120
QY	121	KAYAAFKVSFPLCLTWSITVYAAKGGTSTLANVLSAALLGLTWQCGYLAHDFLHNQV	180
Db	121	kayaafkvsfplcltwsgitvyaawgtsltanvlsaallglftwqcgylaahdflnhqv	180
QY	181	QDRFWGDLFGAFLGVCYCGFSSSSMKWKKNHTNHAAPVHGEDPDIDHPLTLTWEHALEM	240
Db	181	qdrfwgdlfgaflgvcgfgssssmkwkknhtnhaapvnhgedpdidhpltltwehalem	240
QY	241	FSDVPDEELTMMSRFVNLQNTWYPTLSFARLSWGLSTILEVLPNGAHKPSGARVPT	300
Db	241	fsdvpdeeltmmserfvnlqntwyptlsfarlswglstilevlpngahkpsgarvpt	300
QY	301	SLVROLSLAMHNTVYLATMFLFICDPNNMLYVFLVSQAVGNLLATVFSLNHNQMPVISK	360
Db	301	slvrolslamhntvylatmflfikdprnmlyvflvsqavgnllatvflsnhnmpvisk	360
QY	361	EEAVDMDFETKQIITTGGRVHPGLEFANMFSGLANYOIEHNLFPSPMRHNFSKIQPAYETLC	420
Db	361	eeavdmdfetkqiltgdrvhpglfeanfctglnyqiehnlfpsmprhnfskigravetlc	420
QY	421	KKYNVRYHTTGMIGTAEVPSRLNEVSKASKMKCAQ	457
Db	421	kkynvryhttgmigtaeavrsrlnevskaskmkcaq	457

PI	Mukerji P, Huang Y, Parker-barnes JM, Das T;	
DR	WPI; 2000-328935/28.	
XX	DR N-PSDB; AAA09430.	
XX		
PT	Novel transgenic insect cells comprising a nucleotide sequences which	
PT	encode delta-6-desaturase or delta-12- desaturase, useful for producing	
PT	poly-unsaturated long chain fatty acids, e.g. arachidonic acid	
PS		
XX	Claim 1; Page 145-146; 170pp; English.	
XX		
CC	The fatty acid desaturases are able to catalyse the conversion of oleic	
CC	acid to linoleic acid, linoleic acid to gamma-linolenic acid or of	
CC	alpha-linolenic acid to stearidonic acid. Transgenic insect cells	
CC	comprising a nucleotide sequence which encodes a polypeptide comprising	
CC	residues 50-53, 39-43, 172-176, 204-213, or 390-402 of delta-6	
CC	desaturase (AA923599) or comprising delta-12 desaturase (AA192600) are	
CC	claimed. Oil and fatty acids (especially gamma-linolenic acid) isolated	
CC	from the recombinant insect cells are also claimed. Production of	
CC	polyunsaturated long chain fatty acids (PUFAs) in insect cells has many	
CC	advantages, as insect cells have greatly simplified lipid compositions,	
CC	are not subject to external variable fluctuations, and can easily be	
CC	maintained and manipulated. The oils are used in pharmaceutical	
CC	compositions, infant formulas, dietary supplements or substitutes, and	
CC	cosmetics (all claimed). The PUFAs supplements have antiinflammatory,	
CC	antirheumatic, antilastmatic, antipsoptic, osteopathic, cytostatic,	
CC	antidiabetic, dermatological, gynecological, anti-HIV, neuroprotective,	
CC	hypotensive, nephrotoxic, vasodilator, antiagregant and vasotropic	
CC	activity.	
XX		
XX	Sequence 457 AA;	
XX		

RESULT	3
AA992599	
ID	AA92599 standard; Protein; 457 AA.
XX	
AC	AA92599;
XX	
DT	10-AUG-2000 (first entry)
XX	
DE	M. alpina delta-6 fatty acid desaturase.
XX	
KW	delta-6 desaturase; gamma-linolenic acid; biosynthesis;
KW	transgenic insect cell; polyunsaturated long chain fatty acid;
KW	antiinflammatory; antirheumatic; antiasthmatic; antipruritic;
KW	osteopathic; cytosaltic; antidiabetic; dermatological; gynecological;
KW	anti-III; neuroprotective; hypotensive; nephrotropic; vasodilator;
KW	antiaagregant; vasotropic.
XX	
OS	Mortierella alpina.
XX	
XX	
Key	Location/Qualifiers
FT	Misc-difference 172..176
FT	/label="histidine_box
FT	/note="conserved among membrane-bound desaturases"
FT	Misc-difference 209..213
FT	/label="histidine_box
FT	/note="conserved among membrane-bound desaturases"
FT	Misc-difference 395..399
FT	/label="histidine_box
FT	/note="conserved among membrane-bound desaturases"
XX	
PN	WO200020602-A2.
XX	
PD	13-APR-2000.
XX	
PF	29-SEP-1999; 99WO-US22686.
XX	
PR	05-OCT-1998; 98US-0103110.
XX	
PA	(ABBO) ABBOTT LAB.
XX	

Query Match	100.0%	Score 2465	DB 21	Length 457
Best Local Similarity	100.0%	Pred: NO.1.le-245		
Matches 457	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY 1	MAAPSVTRFRAEVLNALNEGKKADEAFGLMTIDDKYVDVREYVDHPGGSYLTHV	60		
Db 1	maapsvtlfraevlnaealneggkkaearflimldnkhydvrefydpbhggsvyllthv	60		
QY 61	GKGDGVDFTRPEAWETLANFYVGDDIDESDRDIKDDFAEVKRLTLFQSLGYDSS	120		
Db 61	gkdgvdftrfpeawetlanfyvgddidesdrdknddfaevkrltlfqslgydas	120		
QY 121	KAYAFKVSFNLCLWGISTVIYAKGQSTLANVLSAALLGLFWOQGLANDPLHHQVF	180		
Db 121	kayafkvsfnlclwglstviyakgqstlanvisaallglfwqcgwlandplfhqvf	180		
QY 181	QDRFNGDLFGAFLGVCQGFSSSMWKDKNHNTHNARNVNGERPDIDTPRLTWSHALEM	240		
Db 181	qdrfngdlfgaflgvcqgfsssmwkdkhntbhaarnvngedrdidtrpiltwschailem	240		
QY 241	FSDVDEELTFMWSFEMVLNTWTFEPLTSFARLSMCOSTLFFVLPRNOAHKPSGARPI	300		
Db 241	fsvdpeelftmwsfemvlnwtwtfepiltstfarslswcqlslftvprnqahkpsgarvpi	300		
QY 301	SLVEQLSLAMHWTWLTATMPLFIKQRPVNLVYFLVSAQVCGNLKLVSLNHNGRPVTSK	360		
Db 301	slveqlslamhwtwlytlaemflfikrprvmllyvflvsqvcgnlllavslnhngprvtsk	360		
QY 361	EEAVYDMDEFTKOITIGRDVNHQGLFANWFTGGILNVOIEHNLFRPSMRHNFSKIQPAVETLC	420		
Db 361	eeavdmdeftqiligtgrdvnhpqlfanwtctgnylgiehlfrpsmrhmfskqpavetlc	420		
QY 421	KKYVRYHTTGMIEGSTAEVFSRLNEVSKAASKMGKAQ	457		
Db 421	kkynvryhttgmiestaevfsrcnlnevskfaaskmgkaq	457		

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XX AAY56045;
AC
XX 28-MAR-2000 (first entry)
DE Fungal delta6-desaturase protein sequence.
XX
XX Polyunsaturated fatty acid; fungus; delta6-desaturase; animal feed;
XX transgenic animal; malnutrition; biosynthesis.
XX
XX Unidentified.
OS
XX WO9961602-A1.
PN
XX 02-DEC-1999.
PD
XX 28-MAY-1999; 99WO-US12088.
PE
XX 29-MAY-1998; 98US-0087578.
PR
XX (OHIO ) UNIV OHIO STATE.
PA
XX Kopechick JJ, Kelder B, Huang Y, Kirchner SJ, Mukerji P;
PI
XX WPI; 2000-072619/06.
DR
XX N-PSDB; AAZ47129.
DR
XX
XX Producing essential fatty acids and long-chain polyunsaturated fatty
PT acids, for use in nutritional, animal feed and medical formulations -
XX
XX Disclosure: Fig 9; 71pp; English.
XX
XX The invention relates to a method of generating novel compositions
CC comprising animal cells producing essential fatty acids (FAs). The animal
CC cells are produced by transforming cells, e.g. embryonic stem cells, with
CC nucleic acid encoding heterologous enzymes involved in fatty acid,
CC e.g. long chain or polyunsaturated fatty acid (PFA) biosynthesis. This
CC sequence corresponds to a fungal delta6-desaturase whose coding sequence
CC is an example of a nucleic acid sequence used to transform the cells. The
CC essential FAs obtained can be used in nutritional formulations or animal
CC feed formulations. The long chain PFAs can be used in nutritional
CC formulations, cosmetic formulations or animal feed formulations. The
CC products can also be used for producing transgenic animals which can be
CC used for producing essential FAs which can be used for producing
CC downstream products such as leukotrienes, thromboxanes, arachidonic acid,
CC eicosapentaenoic acid or docosahexaenoic acid. The products can also be
CC used in cell culture. The animal or milk fat produced can be administered
CC to treat malnutrition.
XX
XX Sequence 457 AA;
SQ

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DB 241 ftdvpdeeltmrmsrfmwlngtlfyfpilstfarlswcigsllfvlpnqgahkpsgavp1 300
OY 301 SLVROLSLAMHMTWYLAITMFLFIKDPVNMVLYFLVSOAVCGTLAIVSLNNGPVS1K 360
DB 301 slveqslslamhwltwylaiflikdpvnmlyvflvsgavcgnllaivslnngpvs1k 360
OY 361 EEAVMDFFTKOILTRGVHPGLFANWFTGILNQIEIHLPPSPMRHNSKIQAVETLC 420
DB 361 eeavmdfftkilgrdvhpplfanwftglnyglehllfpmprhnsksqpavetlc 420
OY 421 KRYNVRHYHTGMIEGTAEVFSRLNEVSKAASKMGKAQ 457
DB 421 kkyvnyhtgmiegtaevfsrlnevskaaskmgkaq 457

RESULT 5
AAB31684
ID AAB31684 standard; Protein; 457 AA.
XX
AC AAB31684;
XX
DT 30-APR-2001 (first entry)
XX
DE Amino acid sequence of a fungal delta6 desaturase.
XX
KW delta6 desaturase; desaturase gene; elongase gene; fatty acid;
KW eicosanoid; nutrition; infant formula; dietary supplement;
KW dietary substitute; animal feed.
XX
XX Mortierella alpina.
XX
OS WO200104636-A1.
XX
PN 18-JAN-2001.
XX
PD 11-JUL-2000; 2000WO-US19011.
XX
PR 12-JUL-1999; 99US-0351525.
XX
PA (UYOH-) UNIV OHIO.
XX
PI Kopechick JJ, Kelder B;
XX
DR WPI; 2001-182622/18.
DR N-PSDB; AAF25234.
XX
XX New compositions comprising cells that express desaturases and
PT elongases, for synthesizing essential fatty acids or long-chain
PT polyunsaturated fatty acids, used in nutritional, cosmetic or animal
PT feed formulations -
XX
XX Disclosure: Fig 9; 93pp; English.
XX
XX The present sequence represents a delta6 desaturase. The desaturase
CC polynucleotide sequence was used to trasfect mammalian cells, to
CC produce animal cells expressing a desaturase gene and/or an elongase
CC gene. Compositions comprising cells of the invention are useful for
CC synthesizing essential fatty acids, their derivatives or downstream
CC products, as well as altered levels of long-chain polyunsaturated
CC fatty acids and eicosanoids. The compositions are useful in nutritional
CC formulae, e.g. infant formula, dietary supplements or dietary
CC substitutes for both humans and animals. The compositions are also
CC useful in cosmetic or animal feed formulations. Furthermore, the
CC compositions may also be used as fat free media or as research reagents.
XX
XX Sequence 457 AA;
SQ

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OY Query Match 100.0%; Score 2465; DB 21; Length 457;
DB Best Local Similarity 100.0%; Pred. No. 1.1e-245;
Matches 457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY Query Match 100.0%; Score 2465; DB 22; Length 457;
DB Best Local Similarity 100.0%; Pred. No. 1.1e-245;
Matches 457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MAAPSVRFTTAEVLNAEALNEGKKDAEAPFLMTIDNKYVDREVPDHPGGSVILTHV 60
DB 1 maapsvrtfttreavlnaealneggkdaaepflmldnkvydrefyphdpbgsvllthv 60
QY 61 GKQDTVFDFPHPEAAWETLANFYVGDIDESDRIKNDDEPAEVRKRLRTFOSIGYDSS 120
DB 61 gkgdtvdfdfphpeaawetlanfyvgdidesdrldknddtaeavrkrlrtlfqslgydss 120
QY 121 KAYFAKVSFNLCTWGLSTIVYVAKWGQSTLANVLSAALLGLFWQCGWLAHDFLHQVF 180
DB 121 kayafkvsfnlctwglstivyakwgqstlanvlsaalglfwqcgwlahdfllhqvf 180
QY 181 QDRFWGDLFGAFLGVCQGGSFSSWMDKHNTHAARVHGEDPDIDTHPLTWSEHALEM 240
DB 181 qdrfwgdlfgaflgvcqggsfsswmdkhnthaaarvvhgedpdidthplltwsehalem 240
QY 241 FSDVPDEELTRMSRFVNLQTFEYFPLISFARLSWCLQSLFLVLPNGQAHKPSGARVP1 300
DB 241 fsdvpedeeltrmsrfvnlqtfefyplisfarlswclqslflvlpngqahkpsgarvp1 300
QY 301 SLVEQSLAMHWMTWYLATMFLFKDVPYMLVYFLVSOAVGNLAIYFSLNHGMPYISK 360
DB 301 slveqslamhwmtwylatmflfkdvpymlvyflvsqavcnllaiyfslnhgmpyisk 360
QY 361 EEAVDMDFTKQIITGSDVHFGLEPAMFTGCLNYQIEHHLFSPMPRHNSKIQPAVETLC 420
DB 361 eeavdmdfctkqiltgsvdhfgllepamftgclnyqiehhlfspmprhnskiqpavetlc 420
QY 421 KKYNVRYHTTGMEGTAEVFSRLNEVSKASKMGKAQ 457
DB 421 kkyinvryhttgmetgaevfsrlnevskaaskmgkaq 457

RESULT 6

AAW85121
AAW85121 standard; Protein; 457 AA.AC AAW85121;
DT 11-FEB-1999 (first entry)
XX

DE A delta-6 desaturase enzyme amino acid sequence.

XX Fatty acid: delta-6 desaturase; polyunsaturated fatty acid;

KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
KW cancer; diabetes; eczema; platelet aggregation; vasodilation;

KW cholesterol level; endometriosis; premenstrual syndrome;

KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
KW acute respiratory syndrome; hypertension; inflammatory skin disorder.

XX Unidentified.

OS

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX The present sequence represents a fatty acid delta-6 desaturase enzyme.
CC The specification describes methods for desaturating a fatty acid and
CC for producing a desaturated fatty acid by expressing increased levels of
CC a desaturase. The present desaturase is an enzyme which introduces a
CC double bond carbons 6 and 7 from the carboxyl end of a fatty acid
CC molecule. The enzyme can be used for desaturating fatty acids. The
CC enzyme can be used to produce polyunsaturated fatty acids, which can
CC be used for treating malnutrition, in pharmaceutical compositions,
CC in cosmetics or in animal feed. The polyunsaturated fatty acids can
CC be used for treating e.g. restenosis after angioplasty, inflammation,
CC rheumatoid arthritis, asthma, psoriasis, cancer, diabetes or eczema
CC or reduce blood pressure. They can also be used to inhibit platelet
CC aggregation, cause vasodilation, lower cholesterol levels, inhibit
CC proliferation of vessel wall smooth muscle and fibrous tissue,
CC reduce or prevent gastro-intestinal bleeding and other side effects
CC caused by non-steroidal anti-inflammatory drugs, prevent or treat
CC endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis
CC and chronic fatigue after viral infections, treat AIDS, multiple
CC sclerosis, acute respiratory syndrome, hypertension and inflammatory skin
CC disorders.
XX
SQ Sequence 457 AA;

Query Match 99.6%; Score 2456; DB 20; Length 457;
Best Local Similarity 99.8%; Pred. No. 9.2e-245;
Matches 456; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAPSVRFTTAEVLNAEALNEGKKDAEAPFLMTIDNKYVDREVPDHPGGSVILTHV 60
DB 1 maapsvrtfttreavlnaealneggkdaaepflmldnkvydrefyphdpbgsvllthv 60
QY 61 GKQDTVFDFPHPEAAWETLANFYVGDIDESDRIKNDDEPAEVRKRLRTFOSIGYDSS 120
DB 61 gkgdtvdfdfphpeaawetlanfyvgdidesdrldknddtaeavrkrlrtlfqslgydss 120
QY 121 KAYFAKVSFNLCTWGLSTIVYVAKWGQSTLANVLSAALLGLFWQCGWLAHDFLHQVF 180
DB 121 kayafkvsfnlctwglstivyakwgqstlanvlsaalglfwqcgwlahdfllhqvf 180
QY 181 QDRFWGDLFGAFLGVCQGGSFSSWMDKHNTHAARVHGEDPDIDTHPLTWSEHALEM 240
DB 181 qdrfwgdlfgaflgvcqggsfsswmdkhnthaaarvvhgedpdidthplltwsehalem 240
QY 241 FSDVPDEELTRMSRFVNLQTFEYFPLISFARLSWCLQSLFLVLPNGQAHKPSGARVP1 300
DB 241 fsdvpedeeltrmsrfvnlqtfefyplisfarlswclqslflvlpngqahkpsgarvp1 300
QY 301 SLVEQSLAMHWMTWYLATMFLFKDVPYMLVYFLVSOAVGNLAIYFSLNHGMPYISK 360
DB 301 slveqslamhwmtwylatmflfkdvpymlvyflvsqavcnllaiyfslnhgmpyisk 360
QY 361 EEAVDMDFTKQIITGSDVHFGLEPAMFTGCLNYQIEHHLFSPMPRHNSKIQPAVETLC 420
DB 361 eeavdmdfctkqiltgsvdhfgllepamftgclnyqiehhlfspmprhnskiqpavetlc 420
QY 421 KKYNVRYHTTGMEGTAEVFSRLNEVSKASKMGKAQ 457
DB 421 kkyinvryhttgmetgaevfsrlnevskaaskmgkaq 457

RESULT 7

AAW84139
AAW84139 standard; Peptide; 355 AA.AC AAW84139;
DT 15-FEB-1999 (first entry)
XX

DE Desaturase enzyme peptide sequence.

XX Fatty acid: desaturase; polyunsaturated fatty acid;

XX

XX

XX

XX

malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
KM cancer; diabetes; eczema; platelet aggregation; vasodilation;
KM cholesterol level; endometriosis; premenstrual syndrome;
KM myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
KM acute respiratory syndrome; hypertension; inflammatory skin disorder.
XX
OS unidentified.
XX
PN WO9846763-A1.
XX
PD 22-OCT-1998.
XX
PF 10-APR-1996; 98MO-US07126.
XX
PR 11-APR-1997; 97US-0834655.
XX
PA (ABBO) ABBOTT LAB.
XX (CALJ) CALGENE LLC.
PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P;
PI Thurmond J;
XX
DR WPI: 1998-594582/50.
XX
PT New isolated fatty acid desaturase enzymes - used for the production
PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical
PT compositions, nutritional compositions, cosmetics or animal feed
PS Example 2; Pages 101-102; 165pp; English.
XX
XX The present sequence represents a peptide derived from a desaturase
CC enzyme. The specification describes methods for desaturating a
CC fatty acid and for producing a desaturated fatty acid by expressing
CC increased levels of a desaturase. Desaturases can be used for
CC desaturating fatty acids. The enzymes can be used to produce
CC polyunsaturated fatty acids, which can be used for treating malnutrition,
CC in pharmaceutical compositions, in cosmetics or in animal feed. The
CC polyunsaturated fatty acids can be used for treating e.g. restenosis
CC after angioplasty, inflammation, rheumatoid arthritis, asthma, psoriasis,
CC cancer, diabetes or eczema or reduce blood pressure. They can also be
CC used to inhibit platelet aggregation, cause vasodilation, lower
CC cholesterol levels, inhibit proliferation of vessel wall smooth muscle
CC and fibrous tissue, reduce or prevent gastro-intestinal bleeding and
CC other side effects caused by non-steroidal anti-inflammatory drugs,
CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic
CC encephalomyelitis and chronic fatigue after viral infections, treat AIDS,
CC multiple sclerosis, acute respiratory syndrome, hypertension and
CC inflammatory skin disorders.
XX
XX Sequence 355 AA:
SQ

Query Match 78.3%; Score 1930; DB 19; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.2e-190;
Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 EVRKRLTLEQSGYDDSAAYAFKVSFNLGSLTVIAVMGQSTLANVLSAALLGL 162
DB 1 evrkrltlfsgsgyddsaayafkvsfnlclwglstvlvawgqstlanvlsaallgl 60
QY 163 FMOQCGMLAHDFLHNOVDFRFGDLFGAFLGVCVCGFSSSMWKDKHNTNHAAPNVHGED 222
DB 61 fmgqcgmlahdfhnovdfrfgdlfgaflgvcvvcgffsssmwkdkhntnhaapnvghed 120
QY 223 PPIIDHPLLTWSEHALENMSDVPDEELTRMSRFVNLQNTWTFYFPLISARLSWCLQSTIL 282
DB 121 ppidhplltwsehalenmsdvpdeeltmwsrfvnlqntwtfyfpilisarswclqstl 180
QY 283 FVLPGOAHKPGGAVRPSILVEQLSLAMHTWYLATMFLFIDPVMNMLYFLVSAVCGN 342
DB 181 fvlpguahkpggavrp silveqlslamhtwylatmflfidpvmnml yflvsaavcgn 240
QY 343 LLAIVESLNHNGMPVISKEADVMDFTFKOITTGRDVHNGFLFANFTGGLNIOIENHLP 402

|||||
DB 241 llaiveslnhngmpviskeadvmdftfkqiltgrdvhngflfanwftgglngyiehlhp 300
QY 403 SMPRHNESTIOPAVENLCKKYNRYHTTGMISTAFVSRLENVSKAASKMKRAQ 457
DB 301 smprhnestio pavenlckkynryhttgmistafv srleenvskaaskmkraq 355

RESULT 8
AAB46440
ID AAB46440 standard. Protein; 520 AA.
XX
XX AAB46440;
XX
DT 06-APR-2001 (first entry)
XX
DE C. purpureus delta6-acetylenase/delta6-desaturase SEQ ID NO 12.
XX
KW Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;
KW cosmetic.
XX
OS Ceratodon purpureus.
XX
PN WO200075341-A1.
XX
PD 14-DEC-2000.
XX
PF 07-JUN-2000; 2000MO-EP05274.
XX
PR 07-JUN-1999; 99DE-1025718.
PR 22-DEC-1999; 99DE-1062409.
XX
PA (BADI) BASF AG.
XX
PI Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehrlinger U;
PI N-PSDB; AAF25734.
XX
DR WPI: 2001-112150/12.
XX
PT Nucleic acid encoding delta6-acetylenase or desaturase, useful for
PT producing plant oils with increased content of unsaturated fatty acids
PT
PS Example 7; Page 57-59; 69pp; German.
XX
XX This invention describes a novel isolated nucleic acid (I) encoding
CC polypeptides (II) with delta6-acetylenase and/or delta6-desaturase
CC activity. The invention also describes (a) amino acid sequences encoded
CC by (I); (b) an expression cassette (EC) containing (I) linked to one or
CC more regulatory sequences; (c) a vector containing (I) and EC; (d)
CC organisms containing (I), EC or the vectors of (c); (e) preparation of
CC unsaturated fatty acids (A) or triglycerides (TG) with increased content
CC of (A) by introducing (I) or EC into an oil-producing organism; (f)
CC proteins (Iia) of 172 aa or 178 aa (given in the specification); (g)
CC production of (A) or TG by using (Iia); and (h) (A) and TG produced by
CC method (g). (I) are used to produce transgenic plants (or other
CC organisms) that produce oils or triglycerides (TG) with increased content
CC of unsaturated fatty acids (A) and to isolate related sequences by
CC homology screening. (A), or TG containing them, are useful in human
CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes,
CC can be used to suppress expression of (II), resulting in oils with
CC increased content of saturated fatty acids.
XX
XX Sequence 520 AA:
SQ

Query Match 35.4%; Score 873; DB 22; Length 520;
Best Local Similarity 43.1%; Pred. No. 2.5e-81;
Matches 185; Conservative 68; Mismatches 134; Indels 42; Gaps 10;

QY 34 MIIIDKKYDVREYVDHFGSVILTHVGKDGVDVDTFPRKAMETLANFYGDIDESDR 93

```
Db 116 lllkkyvdstlaeqhpggvtvntlyfgirdatdvtfstfhastrskllqnfylgnlvreep 175
OY 94 DINKDDAAAEVRKRLTLEFQSLGYDSSKAYAFKVSFNLCIMWGLSTYIVAKMGOTSLAN 153
Db 176 tl---ellkeyreltralfteqlfksksyylfklcllnvalstalslly--ksyavr 230
OY 154 VLSAALLGLFMOOCGLWLANDFLHNOVFQDRFWDLEFGAFGVCQCGSSSMWKDKNHTNH 213
Db 231 llaaslmglftgqgwshdfllnhqvteclwlvdyvgyvgnvylgfsvswkckhnlh 290
OY 214 AARNVHGE-----DPDIDTNPRLTWSEHALEMFSVPDEELTRMWSFVNLQTFEYFPI 268
Db 291 aapnecdqkyptridedidtrilawsk---dlalatesktmlr-----vlyqghlflvl 342
OY 269 LSPFARLSMCLQSLIFVLPNQGAHKPSGARVPISLVEOL-----SLAMHWYLAIMEFLIK 324
Db 343 lltfarsawltwsaafll-----rpecltgekllegrtmalyfwfnsvaltyllp 391
OY 325 --DPVNNLVYFLVSOAVCGNLAIYFSLNHNMPYIKSEEAVIDMDFTKOITRGDVP 382
Db 392 gwnprv---vwmvyselmsgfllygvfvlshmgmevntsk---dfvnaqiasctrdikag 444
OY 383 LFAWNETGGLNYQIEHHLFPSMPRHNSKIQPAVETLCKRYNRYHTTGMIEGTAEVFSR 442
Db 445 vfnodwftglnrgtjehhlfptmprhlnklslshvetlckkhglvgedvmasgtyrvlkt 504
OY 443 LNEYSKAAS 451
Db 505 lkdvadaas 513
```

RESULT 9

AAB46435 standard; Protein: 483 AA.

AAB46435;

06-APR-2001 (first entry)

C. purpureus delta6-acetylenase/delta6-desaturase SEQ ID NO 2.

Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
transgenic plant; plant oil; triglyceride; nutrition; animal feed;
cosmetic.

Ceratonodon purpureus.

WO200075341-A1.

14-DEC-2000.

07-JUN-2000; 2000MO-EP05274.

07-JUN-1999; 99DE-1025718.

22-DEC-1999; 99DE-1062409.

(BADI) BASF AG.

Heinz E, Szymme S, Lee M, Girke T, Sperling P, Zaehringner U;

N-PSDB; AAF25729.

Nucleic acid encoding delta6-acetylenase or desaturase, useful for

producing plant oils with increased content of unsaturated fatty acids

Example 8; Page 44-46; 69pp; German.

This invention describes a novel isolated nucleic acid (I) encoding
polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase
activity. The invention also describes (a) amino acid sequences encoded

CC by (1); (b) an expression cassette (EC) containing (I) linked to one or
CC more regulatory sequences; (c) a vector containing (I) and EC; (d)
CC organisms containing (I), EC or the vectors of (c); (e) preparation of
CC unsaturated fatty acids (A) or triglycerides (TG) with increased content
CC of (A) by introducing (I) or EC into an oil-producing organism; (f)
CC proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)
CC production of (A) or TG by using (Ia); and (Ih) (A) and TG produced by
CC method (g). (I) are used to produce transgenic plants (or other
CC organisms) that produce oils or triglycerides (TG) with increased content
CC of unsaturated fatty acids (A) and to isolate related sequences by
CC homology screening. (A), or TG containing them, are useful in human
CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes,
CC can be used to suppress expression of (II), resulting in oils with
CC increased content of saturated fatty acids.

Sequence 483 AA;

Query Match 34.1%; Score 841.5; DB 22; Length 483;

Best Local Similarity 39.2%; Pred. No 4e-78; Mismatches 159; Indels 43; Gaps 10;

Matches 177; Conservative 72; Mismatches 159; Indels 43; Gaps 10;

9 TPTFAEVLNMEALNEGKKADEAPFLMIIDNKVYDVRFPDPGGSVLTNVGKGTDFV 68

62 tystladv-----aashdrpgdcwmilvkkyvlstfaddhpggvtvlsyfygrgtdvf 113

69 DTFHPEAWEETLANFYGGDDIDESDRDINKDDFAAEVRKRLTLEFQSLGYDSSKAYAFKV 128

114 atfhppaawqgldnyldl---areepdelldydrmaetfregdlfkskawkfllqt 170

129 SFNLCIMWGLSTYIVAKMGOTSLANVLSAALLGLFMOOCGLWLANDFLHNOVFQDRFWDL 188

171 llnaalfaaslatlcy--dksywaivlsaslmglfygqcgyladflnhgvfentansf 228

189 FGAFLEGVCQGFSSSMWKDKNHTNHAARNVHGE-----DPDIDTNPRLTWSEHALEMFS 243

229 fgyllfgncvlgfsvswrktknhlhtapnecdegytrldedidtrilawsk---ellat 285

244 VPDEELTRM--WSRFVNLQNTWTFEFPRLSPARLSMCLQSLIFVL--PQGAHKPSGARVPI 300

286 veskrllrvlyqghymll-----pilmaywstfgslflftnpldstk----- 330

301 SLVQGLSLAMHWYLAIMEFLIKDPVNNLVYFLVSOAVCGNLAIYFSLNHNMPYISK 360

331 gliekgtvalfhawfsaaahllpvgakpklamwateivaglllgvftslhngkeyne 390

361 EEAVMDPFTKOITGRDVHNGLEFANWETGGLNYQIEHHLFPSMPRHNSKIQPAVETLC 420

391 sk---dfvraqvlttrntkrqgfwndvftgldtqiehlhftmprhlnpkrplapqvealc 446

421 KKYNVRHTHTGMIEGTAEVFSRLNEVSKAAS 451

447 kkhgleydnsvvygavavvkalkeadeas 477

RESULT 10

AAB46436 standard; Protein: 483 AA.

AAB46436;

06-APR-2001 (first entry)

C. purpureus delta6-acetylenase/delta6-desaturase SEQ ID NO 4.

Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
transgenic plant; plant oil; triglyceride; nutrition; animal feed;
cosmetic.

Ceratonodon purpureus.

WO200075341-A1.

[illegible]

```

Db      391 sr---dfrraqvltlrntkrigwfnwfctggldtqlqlehlftpmrhnypkrlapgyealc 446
Oy      421 KRYNRYHTTGMIEGTAEVFSRLNEVSKAAS 451
       || : | : : | : | : | : | : |
Db      447 kkhgleydhvsvvgasavavvkalkeladeas 477

RESULT 11
AAVS1354
ID      AAVS1354 standard; Protein: 525 AA.
AC      AAVS1354;
DT      27-APR-2000 (first entry)
DE      Protein b5pp with delta6 fatty acid desaturase activity.
KW      sphingolipid desaturase; sldl; sphingobase; ceramide; capnoid;
KW      transgenic plant; crop plant; delta-8 unsaturated long-chain base;
KW      tolerance; resistance; soil salinity; ion stress; toxicity; drought;
KW      cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
KW      pharmaceutical; food; chemical raw material.
XX      Unidentified.
OS
PN      DEJ9828850-A1.
XX
PD      30-DEC-1999.
XX
PF      27-JUN-1998; 98DE-1028850.
XX
PR      27-JUN-1998; 98DE-1028850.
PA      (GVSE-) GVS GES ERWERB & VERW LANMWIRTSCHAFTLICH.
PI      Heinz E, Zaehrer U, Schmidt H, Sperling P;
DR      WPI; 2000-127549/12.
XX
PT      New sphingolipid desaturase that selectively introduces double bond
PT      into sphingolipids and capnoids -
PS      Disclosure; Fig 16; 62pp; German.
XX
CC      This invention describes a novel sphingolipid desaturase that selectively
CC      introduces a double bond into the sphingobase of the ceramide residue of
CC      sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
CC      desaturase, or a vector containing the DNA sequence, can be used to
CC      produce transgenic plants, especially crop plants, with an increased or
CC      decreased delta-8-unsaturated long-chain base content or an altered
CC      delta-8-unsaturated long-chain base cis/trans ratio, especially to
CC      compensate for a delta-8-unsaturated long-chain base deficiency to
CC      exclude production of delta-8-unsaturated bases, to increase tolerance
CC      or resistance to soil salinity, ion stress or toxicity, drought, wet
CC      conditions, cold or frost and/or phytopathogenic microorganisms, or to
CC      alter size growth and flowering time. Cells, transgenic organisms or
CC      plants containing the DNA sequence can be used to produce sphingolipids
CC      and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
CC      can be used in cosmetics, pharmaceuticals and foods and as chemical raw
CC      materials. This sequence represents a protein which has delta6 fatty acid
CC      desaturase activity which is described in the method of the invention.
XX
SQ      Sequence 525 AA:

Query Match          33.2%; Score 818; DB 21; Length 525;
Best Local Similarity 38.8%; Pred. No. 1.2e-75;
Matches 165; Conservative 86; Mismatches 142; Indels 32; Gaps 10

34 MITDNKYVDREFEVDHGGSGYILRHVGKDGDDVEDTFPEAEAMETLANFYGGDIDESDR 93
   :: ||||| | : ||||| | : ||||| | : | : | : ||||| :
121 lvvknkvysvnfndahdpbgsvistyfgrgdvfssffnaastwkllgdyfgdverve- 179

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OY	94	DIRKDDAAAEVRKLRTEFQSLGYDSSKAYAFKVSFNLCITGSLSTVIVAKKGGPSTLAN	153
Db	180	--ptpelldkfremtraflfreglfksskilywmklltnvalfaasialic-wsktis-av	235
OY	154	VLSAALLGLFMQOCGWLANDFELHHQVFORFPGDILFGAFGLGVCOCGFSSSMWKOKNTHN	213
Db	236	laascmmalctgqgwshphflnngfetrwlnenvgyvlgnaavlgtfstgwwkekhnlhn	295
OY	214	AAPVABGE-----DPDIDHPRLLTWSENALBMSDVPDEELTRMMSRPMVLNQWTFYFPI	268
Db	296	aapnecqcypridedidtlprlawsk---dlalatvenktflr-----llgyqlffmgj	347
OY	269	LSFARLSMCSQSLFVLPNGQAKKPGSARVPIS-LVEQSLSMHMTWYLTATFLEFIKRPV	327
Db	348	lfargswllfws-----wytstlavlsprdrllkxgtvlfhyfwtvgta-cyllpgw	398
OY	328	NMLYFPLVSOAVCGNLIAIVFSLNHNGMSPVISEKEAVDMDFFTKQIITGRDVPGLFANM	387
Db	399	kplvmawetelmstmglwlgfvfvlshngmveynysk-----efvsagivstredtkgnlfdw	454
OY	388	FTGGGLNQIETHLLPPSPMRPHNSKIQPAVEYLCKKYNRYHTTGMIESTAEVFSRLNEVS	447
Db	455	ftgglnrqiehlhflmpmrhnlkraprevfckknglyedvgsiatgcykylaklkeva	514
OY	448	KAASK 452	
Db	515	aaaae 519	
RESULT 12			
ID	AAB46810	standard; Protein; 525 AA.	
AC	AAB46810;		
XX	23-Apr-2001	(first entry)	
DE	P. patens delta6-desaturase protein.		
KW	Delta6-desaturase; unsaturated fatty acid; transgenic; oil; lipid;		
KW	delta6-desat; human nutrition; animal nutrition; cosmetic; pharmaceutical;		
KW	agricultural chemical.		
OS	Physcomitrella patens.		
XX	WO200102591-A1.		
PN	11-Jan-2001.		
PD			
XX	04-JUL-2000; 2000MO-EF06223.		
PF	06-JUL-1999; 99US-0347531.		
XX	30-JUN-2000; 2000DE-1030976.		
PR			
XX	(BAD1) BASF AG.		
PA			
XX	Heinz E, Girke T, Scheffler J, Da Costa Silva EO;		
PI	WPI: 2001-123117/13.		
XX	N-PSDB; NAF26040.		
DR			
XX	Production of unsaturated fatty acids, useful e.g. in nutrition,		
PT	cosmetics or pharmaceuticals, in organisms transformed with		
XX	Physcomitrella patens delta-6-desaturase nucleic acid -		
PS	Claim 1c; Page 41-43; 49pp; German.		
XX			
CC	This invention describes a novel preparation of unsaturated fatty acids		
CC	(I) by introducing into an organism at least one isolated nucleic acid		
CC	(II) that encodes a polypeptide (III) with Delta6-desaturase activity.		
CC	Organisms that contain at least 1 wt.% (I), on total fatty acid content,		
CC	are then selected. (II) is selected from: (a) a 2012 bp sequence (S1),		
CC	defined in the specification, or its equivalents within the degeneracy of		

CC		The generic code; or (b) derivatives of the sequence of (a) that encode a
CC	55	amino acid polypeptide (S2), defined in the specification, or a
CC	525	polypeptide with at least 50% homology with (S2) and practically the same
CC	enzymatic activity.	The invention also describes (1) transgenic organisms
CC	that contain (II); and (2) oils, lipids and fatty acids produced by the	
CC	new method. The oils, lipids and fatty acids produced by the transformed	
CC	organisms are used in human or animal nutrition, cosmetics,	
CC	pharmaceuticals and agricultural chemicals. (III) can also be used, in	
CC	vitro, for increasing the (I) content of triglycerides. The transgenic	
CC	organisms have increased contents of (I), or of (I)-containing	
CC	triglycerides, particularly of gamma-linolenic acid.	
XX		
SQ	Sequence	525 AA;
	Query Match	33.2%; Score 818; DB 22; Length 525;
	Best Local Similarity	38.8%; Pred. No. 1.2e-75;
	Matches 165; Conservative	86; Mismatches 142; Indels 32; Gaps 10;
OY	34	MIDNNKYDVAREPYPDHPGSGVILTHNGKSDTVDFDTPHPEAMETLANFYVGDIIDESDR 93
Db	121	IIVNKKXVDYVSFADENHPSGVLSYFGIGTIDVSSfhaastwklldqdyigderve - 179
OY	94	DIKNDDEAFAEVRKLTLEQSLGYDDSKAYAPFKYSNFLCTMGUSTVVAKKGNSTLAN 153
Db	180	--ptpellkdtremtalflreqliksskilyvmklitvalfaasatlac-wsktis-av 235
OY	154	VLSAALLGLFMQOCGMILAHDLHQVFQDRWCGDLFGAFLGVCQGFSSSMMKDKNTNH 213
Db	236	Iaaacmmlactgqggvashdclfhngvfetrvlnevygyivagnavgifcgywkkehhlnh 295
OY	214	AAPNVHG-----PPDIDTPRLTWSEHALEMFSDPDEBELTRMKSRRMYLNLQTWFYPT 268
Db	296	aapnecdqtyridedictlprllaws--dlatvenktfeir-----llgqhlfmgj 347
OY	269	LSPARLSMCLOSILFVLPRNGAHKPSGARVVIS-LVEDLSAMHNHTWLATMFLEIKRPV 327
Db	348	lffargswlfs-----wryfstavlspvdrllekgtvlfnhyfwtvgta-cyllpwg 398
OY	328	NMLVYFLVSQAVCNLLAIVFSLNHNGMPVTSKEAVDMDFTKOIIIGRDVNPLGFANM 387
Db	399	kplvwmaetelmsgmlllgfvfvlshngeuyvsak----etsaqivatrldkgnjfdnw 454
OY	388	FTGGIANVOIEHHLPSPMRANSKIOPAVETLCCKRYNRVHTTGMIEGTAEVFSRLNEVS 447
Db	455	fctglngliehnlftpmprnhlnkaprvevfckbhjlyvedvatstactcvlkalkeva 514
OY	448	KAAKS 452
Db	515	aaaae 519
RESULT 13		
AA196722		
ID	AA196722 standard; Protein; 422 AA.	
AC	AA196722:	
XX	26-SEP-2000 (first entry)	
DT	E. gracilis fatty acid delta-8 desaturase.	
XX	Fatty acid delta-8 desaturase; polyunsaturated; oil; seed;	
DE	infant formula; dietary supplement.	
XX	Euglena gracilis.	
OS		
XX		
FH	Key Location/Qualifiers	
FT	Misc-difference 20..23	
FT	Misc-difference 146..150	
FT	/label= Hls-box_moult	
TT	Misc-difference 183..187	


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Db 178 lfnryndlaasyfvgnlfigfssggwkeghnvhaatvvgdgdldlvpfyatvaeh1 237
QY 238 LEMFSDVPDEELTRMWSRFVNLQTFEFPILSFARLSKLOSILFVLRPGQAHKPSGAR 237
Db 238 nmysgd-----swvntlfirwghvhwtf--mlpflrlswllgslifv-----sq 278
QY 298 VP-----ISLVQLSLAMHMTWYLATMFLFKDPVNMVLVPLVSAVCGNLLAIYF 348
Db 279 mpcHydyrntaiyegvslhwawslgqly-flpDwstrlmflvshlvvgfllshv 337
QY 349 SLNHNMPVYSKEEAVDMDFFTKOITGRDVHNGLFANMFTGCLNTOIEHNLFPSPMRHN 408
Db 338 tfnhyvvekfalsnmsnyacqlmtrmpgrfidwlgglngyiehlfrmptrhn 397
QY 409 FSKIQPAVETLCKKYNVRYHTTGMIEGTAEVFSRLNEVSAASKMKR 455
Db 398 Intvmpdvkefaaanglpywvddyftgfwlelegfrlnaavaaklck 444

RESULT 15
AA96721
ID AAY96721 standard; Protein; 447 AA.
AC AAY96721;
DT 26-SEP-2000 (first entry)
XX
DE C. elegans fatty acid delta-5-desaturase.
XX
KW Fatty acid delta-5 desaturase; polyunsaturated; oil; seed;
KW Infant formula; dietary supplement.
XX
OS Caenorhabditis elegans.
XX
PN W0200034439-A1.
XX
PD 15-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US28655.
XX
PR 07-DEC-1998; 98US-0111301.
XX
PA (UNITW ) UNITV WASHINGTON STATE RES FOUND.
PI Browse JA, Wallis JG, Watts JL;
XX
DR WPI: 2000-431293/37.
DR N-PSDB: AAA51232.
XX
PT Purified protein having desaturase activity, useful for creating a
XX double-bond between two carbons
XX
PS Claim 3; Fig 6A; 74pp; English.
XX
XX This is the Caenorhabditis elegans fatty acid delta-5 desaturase. The
XX cDNA sequence is useful for recombinant production of the enzyme and for
XX generating transformed host cells and transgenic plants. The desaturase
XX can be used for creating a double-bond between two carbons. In
XX particular, the enzyme is useful for producing polyunsaturated fatty
XX acids and for generating enzyme-specific antibodies useful for
XX identifying desaturases. Oil-seed plants may be engineered to incorporate
XX the enzyme so that the plants produce seed oil rich in fatty acids. The
XX fatty acids could be incorporated usefully into infant formula, foods of
XX all kinds, dietary supplements, nutraceutical and pharmaceutical
XX formulations.
XX
SQ Sequence 447 AA:

```

Query Match 25.5%; Score 629; DB 21; Length 447;
 Best Local Similarity 33.0%; Pred. No. 3; le-56;
 Matches 154; Conservative 76; Mismatches 175; Indels 62; Gaps 13;

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QY 25 KQDAEAPFLMIIDNKVYDVAREFV-PRHGGSVILTHVGKDGTDVDFTH---DEA-AMET 79
Db 4 regeherpfllkldgkwccqiddavrlshprgsalttykmdattvfnthfngskeaywtc 63
QY 80 LANFYGGDIDESRDIKNDNF-----AAEYKR----LRTLEQSLGTYD 118
Db 64 elkkecrpgepeiprdikddpikgidvnmgtfnlsekrsqklnksftdlrmvraeglm 123
QY 119 SSKAYAFKVSFNLCTMGSTVIVAKKGTSTLANVLSAALLGLFMQOGCGLAHDFLHHQ 178
Db 124 gspDfYtrkl-----letlcllfatylgthy-yilpsallmgvawqdgwllhefahng 177
QY 179 VFQDRFVGDLFGAFLGVCQGFSSWMKKDKNNHNAAPVNHGDPDIDTHPL-LTWSEHA 237
Db 178 lfnryndlaasyfvgnlfigfssggwkeghnvhaatvvgdgdldlvpfyatvaeh1 237
QY 238 LEMFSDVPDEELTRMWSRFVNLQTFEFPILSFARLSKLOSILFVLRPGQAHKPSGAR 237
Db 238 nmysgd-----swvntlfirwghvhwtf--mlpflrlswllgslifv-----sq 278
QY 298 VP-----ISLVQLSLAMHMTWYLATMFLFKDPVNMVLVPLVSAVCGNLLAIYF 348
Db 279 mpcHydyrntaiyegvslhwawslgqly-flpDwstrlmflvshlvvgfllshv 337
QY 349 SLNHNMPVYSKEEAVDMDFFTKOITGRDVHNGLFANMFTGCLNTOIEHNLFPSPMRHN 408
Db 338 tfnhyvvekfalsnmsnyacqlmtrmpgrfidwlgglngyiehlfrmptrhn 397
QY 409 FSKIQPAVETLCKKYNVRYHTTGMIEGTAEVFSRLNEVSAASKMKR 455
Db 398 Intvmpdvkefaaanglpywvddyftgfwlelegfrlnaavaaklck 444

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Search completed: August 9, 2001, 20:24:13
 Job time: 247 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 9, 2001, 20:24:21 ; Search time 87.05 Seconds
(without alignments)
694.582 Million cell updates/sec

Title: US-09-367-013b-2
Perfect score: 2465
Sequence: 1 MAAPSVRTFTRAEVLNAEA.....EVFSRLNEYSKASKGKRAQ 457

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMBL_16:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organella:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_unclassified:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2465	100.0	457	3 Q9UVV3	Q9UVV3 mortierella
2	2441	99.0	457	3 Q9UVV3	Q9UVV3 mortierella
3	2429	98.5	457	3 Q9HEV4	Q9HEV4 mortierella
4	2404	97.5	457	3 Q9HEV1	Q9HEV1 mortierella
5	1906	77.3	357	3 Q9HDF4	Q9HDF4 mortierella
6	873	35.4	520	10 Q9LEMG	Q9LEMG ceratodon p
7	841.5	34.1	483	10 Q9LENO	Q9LENO ceratodon p
8	818	33.2	525	10 Q9ZNM2	Q9ZNM2 physcomitrite
9	629	25.5	447	5 Q9XTB7	Q9XTB7 caenorhabdi
10	624.5	25.3	419	10 Q9SMO9	Q9SMO9 euglena gra
11	559	22.7	443	5 Q23221	Q23221 caenorhabdi
12	557	22.6	443	5 Q61388	Q61388 caenorhabdi
13	534.5	21.7	444	4 Q9NYX1	Q9NYX1 hellanthus
14	524.5	21.3	444	4 Q9NYX1	Q9NYX1 homo sapien
15	523.5	21.2	444	4 Q60A27	Q60A27 homo sapien
16	522	21.2	449	10 Q9ZRP7	Q9ZRP7 arabidopsis
17	520.5	21.1	448	10 Q04353	Q04353 borago offi
18	518.5	21.0	448	10 Q9SAU5	Q9SAU5 borago offi
19	512.5	20.8	444	4 Q9NRP8	Q9NRP8 homo sapien

20	506	20.5	447	11 Q9EPV4	Q9EPV4 ratius norv
21	502	20.4	449	10 Q9ZRP8	Q9ZRP8 brassica na
22	497.5	20.2	449	10 Q82348	Q82348 arabidopsis
23	497	20.2	446	10 Q9ZRY9	Q9ZRY9 ricinus com
24	492	20.0	469	10 Q9ZT08	Q9ZT08 triticum ae
25	488.5	19.8	446	10 Q9ZT29	Q9ZT29 arabidopsis
26	478.5	19.4	445	4 Q9Y500	Q9Y500 homo sapien
27	462.5	18.8	449	11 Q9JUE7	Q9JUE7 mus musculu
28	460.5	18.7	446	10 Q9PR82	Q9PR82 borago offi
29	460	18.7	444	4 Q9S664	Q9S664 homo sapien
30	447.5	18.2	444	11 Q9Z0R9	Q9Z0R9 mus musculu
31	445.5	18.1	444	11 Q9Z122	Q9Z122 ratius norv
32	439	17.8	444	13 Q9DEX7	Q9DEX7 brachydanio
33	437.5	17.7	347	2 Q9FC35	Q9FC35 streptomyce
34	431	17.5	523	3 Q9HDC8	Q9HDC8 mucor rouxi
35	422.5	17.1	345	2 Q9X8X4	Q9X8X4 streptomyce
36	416	16.9	444	13 Q9DEX6	Q9DEX6 cyprinus ca
37	386	15.7	422	4 Q9H3G3	Q9H3G3 homo sapien
38	384.5	15.6	350	2 Q9F2M3	Q9F2M3 streptomyce
39	337.5	13.7	311	4 Q9Y3X4	Q9Y3X4 homo sapien
40	306	12.4	467	5 Q9G099	Q9G099 dictyostell
41	297.5	12.1	464	5 Q9Y1W0	Q9Y1W0 dictyostell
42	280.5	11.4	446	3 Q74212	Q74212 mortierella
43	228	9.2	428	5 Q9N9B5	Q9N9B5 leishmania
44	227	9.2	368	2 Q54795	Q54795 spirulina p
45	212	8.6	352	4 Q60426	Q60426 homo sapien

ALIGNMENTS

RESULT 1

Q9UVV3 ID Q9UVV3 PRELIMINARY: PRT: 457 AA.

AC Q9UVV3; 01-MAY-2000 (TREMBL) 13, Created)

DT 01-MAY-2000 (TREMBL) 13, Last sequence update)

DT 01-MAR-2001 (TREMBL) 16, Last annotation update)

DE DELTA-6 FATY ACID DESATURASE.

Query Match 100.0%; Score 2465; DB 3; Length 457;
Best Local Similarity 100.0%; Pred. No. 3.9e-218;
Matches 457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPSVRTFTRAEVLNAEALNEGKDAEPFLMIDNKVYDVEEPVDRHGGSYILTHV 60
DB 1 MAAPSVRTFTRAEVLNAEALNEGKDAEPFLMIDNKVYDVEEPVDRHGGSYILTHV 60
QY 61 GKSDTDFDFTFHPAAMETLANFYVGIDIESDRDIKNDFAAEYRKLRTLFQSLGYDSS 120

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|||||
Db 61 GKGDTVPFTFPEAAMETLANFYVGDIDESDRDINKNDFAEVRKRLTFLFOSLGYYDSS 120
OY 121 KAYYAKVSVFNLCIMGLSTVIYAKWGQSTLANVLSAALLGLFWQCGMLAHDFLHHQVF 180
Db 121 KAYYAKVSVFNLCIMGLSTVIYAKWGQSTLANVLSAALLGLFWQCGMLAHDFLHHQVF 180
OY 181 ODREWMDLFGAFLGVCQCGFSSMMWKDKNTHHAAPNVGDEPDIDTHPLTWSEHALEM 240
Db 181 ODREWMDLFGAFLGVCQCGFSSMMWKDKNTHHAAPNVGDEPDIDTHPLTWSEHALEM 240
OY 241 FSDVPDEELTRMMSRPMVLTQWTFYFPLISFARLSWCLQSLIFVLDPNGAHRKPSGARVP1 300
Db 241 FSDVPDEELTRMMSRPMVLTQWTFYFPLISFARLSWCLQSLIFVLDPNGAHRKPSGARVP1 300
OY 301 SLVEQSLAMHMTWYLATMFLFKDPVNNLVYFLVSOAVCGNLATVFSLNHNGMPVISK 360
Db 301 SLVEQSLAMHMTWYLATMFLFKDPVNNLVYFLVSOAVCGNLATVFSLNHNGMPVISK 360
OY 361 EEAVDMDFTKQITTRDVPNGLFANMFTGGLNYQIEHHLPSPMRHNSKIOPAVETLC 420
Db 361 EEAVDMDFTKQITTRDVPNGLFANMFTGGLNYQIEHHLPSPMRHNSKIOPAVETLC 420
OY 421 KRYNRYHTTGMEGTAEVFSRLNEVSKAASKMGKAQ 457
Db 421 KRYNRYHTTGMEGTAEVFSRLNEVSKAASKMGKAQ 457
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RESULT 2
OQ0UVY3 PRELIMINARY; PRT; 457 AA.
AC OQ0UVY3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE DELTA-6 FATTY ACID DESATURASE.
OC Mortierella alpina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae;
OC Mortierella.
OX NCBI_TaxID=64518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1S-4;
RX MEDLINE=20035749; PubMed=10570972;
RT Sakurada et al., Kobayashi M., Shimizu S.;
RT "Delta-6-Fatty acid desaturase from an arachidonic acid-producing
RT Mortierella fungus. Gene cloning and its heterologous expression in a
RT fungus, Aspergillus."
RL Gene 238:445-453(1999).
CC -1- SIMILARITY: TO CYTOCHROME B5 DOMAIN.
DR EMBL; AB020032; BAA85588.1; -.
DR HSSP; P04166; 1B5M.
DR InterPro; IPR001199; -.
DR Pfam; PF00173; heme_L; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; UNKNOW.N.1.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 457 AA; 51816 MW; 5CAB3D7312439543 CRC64;
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Query Match 99.0%; Score 2441; DB 3; Length 457;
Best Local Similarity 98.7%; Pred. No. 6, 2e-216;
Matches 451; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
OY 1 MAAAPSVRTFTRAEVINAALNEGKKDAEPFLMIITDNKYVDYREVPDPHGGSVTLTHV 60
Db 1 MAAAPSVRTFTRAEVINAALNEGKKDAEPFLMIITDNKYVDYREVPDPHGGSVTLTHV 60
OY 61 GKGDTVPFTFPEAAMETLANFYVGDIDESDRDINKNDFAEVRKRLTFLFOSLGYYDSS 120
Db 61 GKGDTVPFTFPEAAMETLANFYVGDIDESDRDINKNDFAEVRKRLTFLFOSLGYYDSS 120
OY 121 KAYYAKVSVFNLCIMGLSTVIYAKWGQSTLANVLSAALLGLFWQCGMLAHDFLHHQVF 180
Db 121 KAYYAKVSVFNLCIMGLSTVIYAKWGQSTLANVLSAALLGLFWQCGMLAHDFLHHQVF 180
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Db 121 KAYYAKVSVFNLCIMGLSTVIYAKWGQSTLANVLSAALLGLFWQCGMLAHDFLHHQVF 180
OY 181 ODREWMDLFGAFLGVCQCGFSSMMWKDKNTHHAAPNVGDEPDIDTHPLTWSEHALEM 240
Db 181 ODREWMDLFGAFLGVCQCGFSSMMWKDKNTHHAAPNVGDEPDIDTHPLTWSEHALEM 240
OY 241 FSDVPDEELTRMMSRPMVLTQWTFYFPLISFARLSWCLQSLIFVLDPNGAHRKPSGARVP1 300
Db 241 FSDVPDEELTRMMSRPMVLTQWTFYFPLISFARLSWCLQSLIFVLDPNGAHRKPSGARVP1 300
OY 301 SLVEQSLAMHMTWYLATMFLFKDPVNNLVYFLVSOAVCGNLATVFSLNHNGMPVISK 360
Db 301 SLVEQSLAMHMTWYLATMFLFKDPVNNLVYFLVSOAVCGNLATVFSLNHNGMPVISK 360
OY 361 EEAVDMDFTKQITTRDVPNGLFANMFTGGLNYQIEHHLPSPMRHNSKIOPAVETLC 420
Db 361 EEAVDMDFTKQITTRDVPNGLFANMFTGGLNYQIEHHLPSPMRHNSKIOPAVETLC 420
OY 421 KRYNRYHTTGMEGTAEVFSRLNEVSKAASKMGKAQ 457
Db 421 KRYNRYHTTGMEGTAEVFSRLNEVSKAASKMGKAQ 457
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RESULT 3
OQHEV4 PRELIMINARY; PRT; 457 AA.
AC OQHEV4;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE DELTA6-FATTY ACID DESATURASE.
OC Mortierella isabellina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae;
OC Mortierella.
OX NCBI_TaxID=91625;
RN [1]
RP SEQUENCE FROM N.A.
RA Ming-Chun L., Li L., Guo-Wu H., Li Z., Lai-Jun X.;
RT "Cloning and sequencing analysis of delta6-fatty acid desaturase gene
RT from Mortierella isabellina."
RT Junwu Xitong 0:0-0(2001).
DR EMBL; AF306634; AAG38104.1; -.
SQ SEQUENCE 457 AA; 51772 MW; 868E7EB21172D5AF CRC64;
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Query Match 98.5%; Score 2429; DB 3; Length 457;
Best Local Similarity 98.5%; Pred. No. 7, 9e-215;
Matches 450; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
OY 1 MAAAPSVRTFTRAEVINAALNEGKKDAEPFLMIITDNKYVDYREVPDPHGGSVTLTHV 60
Db 1 MAAAPSVRTFTRAEVINAALNEGKKDAEPFLMIITDNKYVDYREVPDPHGGSVTLTHV 60
OY 61 GKGDTVPFTFPEAAMETLANFYVGDIDESDRDINKNDFAEVRKRLTFLFOSLGYYDSS 120
Db 61 GKGDTVPFTFPEAAMETLANFYVGDIDESDRDINKNDFAEVRKRLTFLFOSLGYYDSS 120
OY 121 KAYYAKVSVFNLCIMGLSTVIYAKWGQSTLANVLSAALLGLFWQCGMLAHDFLHHQVF 180
Db 121 KAYYAKVSVFNLCIMGLSTVIYAKWGQSTLANVLSAALLGLFWQCGMLAHDFLHHQVF 180
OY 181 ODREWMDLFGAFLGVCQCGFSSMMWKDKNTHHAAPNVGDEPDIDTHPLTWSEHALEM 240
Db 181 ODREWMDLFGAFLGVCQCGFSSMMWKDKNTHHAAPNVGDEPDIDTHPLTWSEHALEM 240
OY 241 FSDVPDEELTRMMSRPMVLTQWTFYFPLISFARLSWCLQSLIFVLDPNGAHRKPSGARVP1 300
Db 241 FSDVPDEELTRMMSRPMVLTQWTFYFPLISFARLSWCLQSLIFVLDPNGAHRKPSGARVP1 300
OY 301 SLVEQSLAMHMTWYLATMFLFKDPVNNLVYFLVSOAVCGNLATVFSLNHNGMPVISK 360
Db 301 SLVEQSLAMHMTWYLATMFLFKDPVNNLVYFLVSOAVCGNLATVFSLNHNGMPVISK 360
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QY 361 EAADMDFFTKOITGRDVHGLFANMFTGGLNTOIEHNLPRSPRHNFSKIOPAVETLC 420
 DB 361 EAADMDFFTKOITGRDVHGLFANMFTGGLNTOIEHNLPRSPRHNFSKIOPAVETLC 420
 QY 421 KKYVRYHTTGMIGSTAEVFSRLNEVSKAASKMGKAQ 457
 DB 421 KKYVRYHTTGMIGSTAEVFSRLNEVSKAASKMGKAQ 457
 RESULT 4
 Q9HEV1 PRELIMINARY; PRT; 457 AA.
 AC Q9HEV1
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE DELTA 6-FATTY ACID DESATURASE.
 OS Mortierella alpina.
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae;
 OC Mortierella.
 NCBI_Taxid=64518;
 RN [1]
 RP SEQUENCE FROM N. A.
 RA Xing L., Li M., Liu L., Hu G., Zhang L.;
 RT "Expression of Mortierella alpina delta 6-fatty acid desaturase gene
 in Saccharomyce cerevisiae.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF307940; AAC45092.1; -;
 SO SEQUENCE 457 AA; 51885 MW; 4B0AC0DD15D19DA1 CRC64;

Query Match 97.5%; Score 2404; DB 3; Length 457;
 Best Local Similarity 98.0%; Pred. No. 1.6e-212;
 Matches 448; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 QY 1 MAAPSVRTFRAEVLNNALENEGKKAADAPLMIIDNKYVDVREVPDHPGGSVILTHV 60
 DB 1 MAAPSVRTFRAEVLNNALENEGKKAADAPLMIIDNKYVDVREVPDHPGGSVILTHV 60
 QY 61 GKDGVDVDFTHPEAAMETLANFYGGDIDESDRAIKNDFAEYKRLTFLQSLGYDSS 120
 DB 61 GKDGVDVDFTHPEAAMETLANFYGGDIDESDRAIKNDFAEYKRLTFLQSLGYDSS 120
 QY 121 KAYAFKSFNCTIGLSTVIYAKWGOTSTLANVLSAALLGLFMQCGMLAHDFLHGV 180
 DB 121 KAYAFKSFNCTIGLSTVIYAKWGOTSTLANVLSAALLGLFMQCGMLAHDFLHGV 180
 QY 181 QDRFWDGLFAGFLGVCQGFSSSMWKDKNTHNHAAPNVHGEDPDIOTHPRLTWSEHALEM 240
 DB 181 QDRFWDGLFAGFLGVCQGFSSSMWKDKNTHNHAAPNVHGEDPDIOTHPRLTWSEHALEM 240
 QY 241 FSDVPDEELTMMSRFMYLNTWTFYFPLISFARLSWCLOSILFVLPNGCAHKPSGARVPI 300
 DB 241 FSDVPDEELTMMSRFMYLNTWTFYFPLISFARLSWCLOSILFVLPNGCAHKPSGARVPI 300
 QY 301 SLVEQLSLAMHMTWYLATMFLFIKDPVNMUYFLVSQAVCGNLLATVSLNHNGMPVLSK 360
 DB 301 SLVEQLSLAMHMTWYLATMFLFIKDPVNMUYFLVSQAVCGNLLATVSLNHNGMPVLSK 360
 QY 361 EAADMDFFTKOITGRDVHGLFANMFTGGLNTOIEHNLPRSPRHNFSKIOPAVETLC 420
 DB 361 EAADMDFFTKOITGRDVHGLFANMFTGGLNTOIEHNLPRSPRHNFSKIOPAVETLC 420
 QY 421 KKYVRYHTTGMIGSTAEVFSRLNEVSKAASKMGKAQ 457
 DB 421 KKYVRYHTTGMIGSTAEVFSRLNEVSKAASKMGKAQ 457

RESULT 5
 Q9HEV1 PRELIMINARY; PRT; 357 AA.
 AC Q9HEV1
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE DELTA 6-FATTY ACID DESATURASE.
 OS Mortierella alpina.
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae;
 OC Mortierella.
 NCBI_Taxid=64518;
 RN [1]
 RP SEQUENCE FROM N. A.
 RA Xing L., Li M., Liu L., Hu G., Zhang L.;
 RT "Expression of Mortierella alpina delta 6-fatty acid desaturase gene
 in Saccharomyce cerevisiae.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF307940; AAC45092.1; -;
 SO SEQUENCE 457 AA; 51885 MW; 4B0AC0DD15D19DA1 CRC64;

DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE DELTA 6-FATTY ACID DESATURASE (FRAGMENT).
 OS Mortierella alpina.
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae;
 OC Mortierella.
 NCBI_Taxid=64518;
 RN [1]
 RP SEQUENCE FROM N. A.
 RA Xing L., Li M., Liu L., Hu G.;
 RT "Cloning and sequence analysis of the conserved region of delta 6-
 fatty acid desaturase gene from Mortierella alpina.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N. A.
 RA Xing L., Li M., Liu L., Hu G., Zhang L.;
 RT "Cloning and sequence analysis of the conserved region of delta 6-
 fatty acid desaturase gene from Mortierella alpina.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF307942; AAC45094.1; -;
 DR EMBL: AF307941; AAC45093.1; -;
 FT NON_TER 1
 FT 357 357
 SO SEQUENCE 357 AA; 40796 MW; C8D9CE1283B16B8 CRC64;

Query Match 77.3%; Score 1906; DB 3; Length 357;
 Best Local Similarity 98.0%; Pred. No. 6.6e-167;
 Matches 350; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 QY 46 FVPDHPGGSVILTHVKGKGTVDVDFTHPEAAMETLANFYGGDIDESDRAIKNDFAEVR 105
 DB 1 FVPDHPGGSVILTHVKGKGTVDVDFTHPEAAMETLANFYGGDIDESDRAIKNDFAEVR 105
 QY 106 KLRTLFOSLGYDSSKAYAFKVSFNCTIGLSTVIYAKWGOTSTLANVLSAALLGLFMQ 165
 DB 61 KLRTLFOSLGYDSSKAYAFKVSFNCTIGLSTVIYAKWGOTSTLANVLSAALLGLFMQ 120
 QY 166 QCGWLADHFLHNOVFQDFEWDGLFGARLGGVCGGSSSMWKDKNTHNHAAPNVHGEDPDI 225
 DB 121 QCGWLADHFLHNOVFQDFEWDGLFGARLGGVCGGSSSMWKDKNTHNHAAPNVHGEDPDI 180
 QY 226 DTHPLTWSEHALEMFSVDPDEELTRMWSRFMYLNTWTFYFPLISFARLSWCLOSILFVL 285
 DB 181 DTHPLTWSEHALEMFSVDPDEELTRMWSRFMYLNTWTFYFPLISFARLSWCLOSILFVL 240
 QY 286 PNGAHRKPSGARVPISLVEQLSLAMHMTWYLATMFLFIKDPVNMUYFLVSQAVCGNLLA 345
 DB 241 PNGAHRKPSGARVPISLVEQLSLAMHMTWYLATMFLFIKDPVNMUYFLVSQAVCGNLLA 300
 QY 346 IVFSLNHNGMPVLSKEEAVDMDFFTKOITGRDVHGLFANMFTGGLNTOIEHNLFP 402
 DB 301 IVFSLNHNGMPVLSKEEAVDMDFFTKOITGRDVHGLFANMFTGGLNTOIEHNLFP 357

RESULT 6
 Q9LEM9 PRELIMINARY; PRT; 520 AA.
 AC Q9LEM9
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE DELTA 6-FATTY ACID DESATURASE.
 OS Ceratodon purpureus (Moss).
 OC Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida;
 OC Dicranidae; Dicranales; Ditrichaceae; Ceratodon.
 OC NCBI_Taxid=3225;
 RN [1]
 RP SEQUENCE FROM N. A.
 RA STRAIN-WT3; TISSUE=PROTONEMATA;
 RX MEDLINE=20307617; Pubmed=10848999;
 RA Sperling P., Lee M., Girke T., Zaehring U., Stymer S., Heinz E.;

RT "A bifunctional delta 6-fatty acyl acetylase/desaturase from the
RT moss *Ceratodon purpureus*. A new member of the cytochrome b5
RT superfamily."
RL Eur. J. Biochem. 267:3801-3811(2000).
DR EMBL: AJ250735; CAB94993.1; -
DR InterPro: IPR001199; -
DR Pfam: PF00173; heme_1; 1.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
SQ SEQUENCE 520 AA: 59160 MW: 5A9332EECC153439 CRC64;

Query Match 35.4%; Score 873; DB 10; Length 520;
Best Local Similarity 43.1%; Pred. No. 1e-71;
Matches 185; Conservative 68; Mismatches 134; Indels 42; Gaps 10;

QY 34 MILDNKYDREVPRDPHGGSVLLTHGKDGTDVDFEPEAAEETLANVYGDDIDESDR 93
DB 116 IIRKEKYDSTAEQHPGGTINTYFGDPTVFTFHASTSMKILQNFYIGNLVREEP 175
QY 94 DIKNDEFAAEVRKRLTFLQSLGYDSSKAYAFKVSFNLCTWGLSTVYAKMGQTSFLAN 153
DB 176 TL---ELKKYRELRLALFLBQFLFKSSKYYLTKTLINSVATSTAIISLY--KSTRAY 220
QY 154 VLSAALLGLFMQCGWLADHLHNOVFQDRFWGDLFGALFGVCOGFSSSMMKDKNTHH 213
DB 231 LLSASLMLGLFIQCCGMLSHDFLHHOYETRWLNDVGYGVGNVVLGFSVMMKTKHNLH 290
QY 214 AARNVHE---DPRDTHPLTLTWSHALFMSDVPDEELTRMSKFFVNLNTWTFEPI 268
DB 291 AARNEDCQKTPIDEDIDTPIILAMSG--DLATVESKTMLR---VLQYOHLEFVL 342
QY 269 LSEFARLSMCLQSLIFVLNPGCAHPSGARVPSILVEQL---SLAMHWYALTMLEFIK 324
DB 343 LTPARASWMLFMSAFTL-----REPLTGERKLEBGRMALHYTPNSVAEFLLP 391
QY 325 --DPVNMVLYEIVSOAVCGNLAIVPSLNHNGMPVISKEEAVDMDEFTKOITGRDVHPG 382
DB 392 GMRPV---VMMVVSSELMSCGLLGYFVFLSHNGMEVYVTSK---DFVNAQIASTRIDIKAG 444
QY 383 LFNANPFGCLNYQIEHNLFPSPRNHNSKIQPAVENTLCKKYNRYHHTGIEGTAEVFSR 442
DB 445 VFNDMFPGCLNROIENHLFPTMPRHNLKISIPVETLCKKHGLVEDVSNASGTYRVLKT 504
QY 443 LNEVSKAAS 451
DB 505 LKDVADAAS 513

RESULT 7
Q9LENO PRELIMINARY: PRT: 483 AA.
AC Q9LENO;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE DELTA 6-FATTY ACETYLENASE.
OS Ceratodon purpureus (Moss).
OC Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida;
OC Dictyidae; Dictyales; Dictyaceae; Ceratodon.
ON NCBI_TaxId=3225;
RX SEQUENCE FROM N.A.
RC STRAIN=WT3; TISSUE=PROTONEMATA;
RX MEDLINE=20307617; PubMed=10848999;
RA Speilung P., Lee M., Gilke T., Zaehring U., Styeme S., Heinz E.;
RT "A bifunctional delta 6-fatty acyl acetylase/desaturase from the
RT moss *Ceratodon purpureus*. A new member of the cytochrome b5
RT superfamily."
RL Eur. J. Biochem. 267:3801-3811(2000).
DR EMBL: AJ250734; CAB94992.1; -
DR InterPro: IPR001199; -
DR Pfam: PF00173; heme_1; 1.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.

SQ SEQUENCE 483 AA: 54857 MW: C451D042169ABIC2 CRC64;

Query Match 34.1%; Score 841.5; DB 10; Length 483;
Best Local Similarity 39.2%; Pred. No. 7.2e-69;
Matches 177; Conservative 72; Mismatches 159; Indels 43; Gaps 10;

QY 9 TPTRAVLAINEALNECKKAEAPFLMIDNKYDVDFEPRDPHGGSVLLTHGKDGTDVFE 68
DB 62 TYSLADV-----ASHDRPGDCMMIVKEKYVDISRFADPHGGTIVSTYFGDGTDFV 113
QY 69 DTFEPRAEATLANFYVGDIDESDRDIKNDEFAAEVRKRLTFLQSLGYDSSKAYAFV 128
DB 114 ATTHPRPAAMQLNDYIIGDL---AREPELDELKQYRDMRAEVRGRGLFKSSAMFLQY 170
QY 129 SFNLCITWGLSTVIVAKGQTSFLANVLSAALLGLFMQCGWLADHLHNOVFQDRFWGDL 188
DB 171 LIMAALFAASIAIACY--DKSYWAIYLSASIMGLFYQCCGWLADHLHQVFEENRTANSF 228
QY 189 FGAFLGVCQCGFSMMKDKNTHHAAPNVHG-----DPDIDTHPLTWSHALFMSD 243
DB 229 FGFLFGCVLGFSSVSMWRKHNHHTAPNECDQYRPLDEIDTPIILAMSK---ELIAT 285
QY 244 VPDEELTRM--NSRFVNLQNTWTFEPILSFARLSMCLQSLIFVL--PNGCAHPSGARVPI 300
DB 286 VESKRLIRVLQYGHMIL-----PLTFMARSMTFSGSLFFFNFDLSYTK----- 330
QY 301 SLVEQLSLAMHWYALTMLEFIKDPVNMVLYFVSQAVCGNLAIVPSLNHNGMPVISK 360
DB 331 GLTEKGTVAHFVAMFMAAFHILPGVAKPLAMVAVATLAVGLLGYFVFLSHNGKELYNE 390
QY 361 EEAVDNDEFKQITGRDVHPGLFANPFGCLNYQIEHNLFPSPRNHNSKIQPAVENTLC 420
DB 391 SK---DFVRAQYITTRNTRKGFNDMFTGGDLTOEHLFPTMPRHNPYKIAPOVEALC 446
QY 421 KKYNVRYHTTGMIECTAEVFSRLNEVSKAAS 451
DB 447 KRHLGEYDVSVGVASVAVYKALKEIADNAS 477

RESULT 8
Q9ZNMW2 PRELIMINARY: PRT: 525 AA.
AC Q9ZNMW2;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE DELTA6-ACYL-LIPID DESATURASE.
GN DES6.
OS Physcomitrella patens (Moss).
OC Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida;
OC Funariidae; Funariales; Funariaceae; Physcomitrella.
ON NCBI_TaxId=3218;
RX SEQUENCE FROM N.A.
RC STRAIN=HEM. B. S. G.;
RX MEDLINE=98416756; PubMed=9744093;
RA Gilke T., Schmidt H., Zaehring U., Reski R., Heinz E.;
RT "Identification of a novel delta 6-acyl-group desaturase by targeted
RT gene disruption in *Physcomitrella patens*."
RL Plant J. 15:39-48(1998).
CC -1- SIMILARITY: TO CYTOCHROME B5 DOMAIN.
DR EMBL: AJ222981; CA11033.1; -
DR EMBL: AJ222980; CA11032.1; -
DR HSSP: P04166; 1B5M.
DR InterPro: IPR001199; -
DR Pfam: PF00173; heme_1; 1.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KM Heme.
SQ SEQUENCE 525 AA: 59369 MW: 530F158B0C97C83F CRC64;

Query Match 33.2%; Score 818; DB 10; Length 525;

Matches 150; Conservative 75; Mismatches 171; Indels 59; Gaps 12;

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OY 23 EKKKQAEPLMIIDKKVDREFVDHGGG-VILTHCKDSTDVDFTHPEAAHETL- 80
DB 2 KSKROLSTPLQML-BQTYDVNF---HPGAEIENYQGRDXTDAFMVHNEAFDCK 56
OY 81 -----ANFVY--GDIDESRDIKNDFAAEYKRLTLEFSGYDSSKAYAFVSEFN 131
DB 37 RMKINPSFELPQOAVNNEQEDF-----RKURELIATGMDDASLWVSYKISTT 107
OY 132 LCTWIGLSTVIVAKGQSTSLANVLSAALLGLFWQCGWLAFHDFLHQVDFRWDLFGA 191
DB 108 LGIGVGLGYFLMVOYQM-----YFIGAVLLGMHVOQMGLSHDICHQTEKRNMMNLVGL 162
OY 192 FLGCGCGGSSSWMKDKHNTHHAAPVHGEDPIDTHPLTWEHALMFMSDVPDELTFR 251
DB 163 VFGNGIAGSFSVTCWKDRHNAHNSATVQGHDPIDMLPLAMSEDDVTRASPI----- 215
OY 252 MMSRFVNLQWTFEPPLISFARLSMCLQSLFVLP-----NGQAHKPGARVPISLVEOLS 307
DB 216 --SRKLIQFOQYFLVLCILRLFTWCFCVLTFRSLKDRNQYRQYKK-----EATG 267
OY 308 LAMHWIYLAETMFLTKDPVNMVYFLVSOAVCGNLATVFSLNHGMPIYSKEEAVDMD 367
DB 268 LALHMTLKLALFHLFMPISITSLVFEFVSELVGFGLAIYVFNHYPLEKIGDPVMDHG 327
OY 368 FFKQIITGDRVHGLFANMFTGGLNVOIEHHLPSPMRHNSKIQPAVETLCKKYNRY 427
DB 328 FSVGQIHEHNMNIRGLITTDWFEGLNVOIEHHLPPLPRNLITAVSYOVELCOKHNLPL 387
OY 428 HTTGMEGTA-----EVSRLNEVSKASKMGKA 456
DB 388 RNLPHREGVLILLRLYLAFAFMAEKQPA-----GKA 418

RESULT 11
OY 023221 PRELIMINARY; PRT: 443 AA.
ID 023221;
AC 023221;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE W0802.4 PROTEIN.
GN W0802.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN 11
RP SEQUENCE FROM N.A.
RA Smithburne J., Ainscough R.;
RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
RN 12
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology."
RT Science 282:2012-2018(1998).
RL EMBL: Z70271; CAA94233.2; -.
DR InterPro: IPR000566; -.
DR InterPro: IPR001199; -.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
DR PROSITE: PS00213; LIPOCALIN; UNKNOWN_1.
SQ SEQUENCE 443 AA; 51772 MW; 9513D61IECB99A06 CRC64;

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Query Match 22.7%; Score 559; DB 5; Length 443;

Best Local Similarity 32.1%; Pred. No. 5.9e-43;

Matches 143; Conservative 64; Mismatches 187; Indels 52; Gaps 11;

OY 34 MIIDNK-VYDVREFFVDHGGGVILTHVKGDKGVDVDFTHPEAAW----- 77

DB 12 MKVDGKMLVLSSELYKKHGGAVIEQYRNSDATHTHPAHFEGSSQAYKOLDLKKHGEHD 71

OY 78 EPLIANVYGDIDESDDINDDEFA-AEVRKRLTPQSL-----GYDSSKAYFAFKS 129

DB 72 EFLEKOLEKRLDKVDLINVSAVDVSAOEKRMVESFEKRLQKLDHDLMAKANEYLFLEKAI 131

OY 130 FNICIGLSTVI-VAKMGQSTSLANVLSAALLGLFWQCGWLAFHDFLHQVDFRWDL 188

DB 132 STLSINAFNFIQYLOLW-----YITSACLALANMQCGWLHHECHQCPKRNRLNT 184

OY 189 FGAFGLGCGGSSSWMKDKHNTHHAAPVHGEDPIDTHPLTWEHALMFMSDVPDEE 248

DB 185 ISLFFGNFLGGSFSDMKKRNHNTHAATVNIHDDGIDIALP-----FAFIPG-D 233

OY 249 LTFPMWSRF-----VYLNQWTFEPPLISFARLSMCLQSLFVLPNGQAHKPGARVPISL 302

DB 234 LCKYKASFERKAIKIVPYOHLFTFALPMLRFSWTCQSVQWFKENQMEKYQR--NAF 291

OY 303 VEOQLSAMHWIYLAETMFLFIKDPVNMVYFLVSOAVCGNLATVFSLNHGMPIYSKEE 362

DB 292 WEGATIVGHMAWVYQFLFLTPWPLR-VAFPIISQGGGLLTAHYTFHNNSVDKYPANS 350

OY 363 AYDMDFEQIITGDRVHGLFANMFTGGLNVOIEHHLPSPMRHNSKIQPAVETLCKK 422

DB 351 RIINNEPALQIILTRRMTPSPFIDWLMGLNVOIEHHLPPLPRNCLNACMKYVEMCKE 410

OY 423 YNRYHTTGMEGTAFAVFSRLNEVSK 448

DB 411 NNLPLVLDVDFDGYAMNLOOLKNMAE 436

RESULT 12

ID 061388 PRELIMINARY; PRT: 443 AA.

AC 061388;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-AUG-1998 (TREMBLrel. 07, last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)

DE DELTA6-FAATY-ACID-DESATURASE.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Pelodierinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN 11

RP SEQUENCE FROM N.A.

RA Sayanova O., Smith M.A., Lapinskas P., Stobart A.K., Dobson G.,

RA Napier J.A., Hey S.J., Lacey D.J., Shewry P.R.;

RT "Identification of a Caenorhabditis elegans Delta6-fatty-acid-

RT desaturase by heterologous expression in Saccharomyces cerevisiae.";

RL Biochem. J. 330:0-0(0).

DR EMBL: AF031477; AAC15586.1; -.

DR InterPro: IPR000566; -.

DR InterPro: IPR001199; -.

DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.

DR PROSITE: PS00213; LIPOCALIN; UNKNOWN_1.

SQ SEQUENCE 443 AA; 51740 MW; 9513CA7C5A7E9A06 CRC64;

Query Match 22.6%; Score 557; DB 5; Length 443;

Best Local Similarity 32.1%; Pred. No. 9.1e-43;

Matches 143; Conservative 64; Mismatches 187; Indels 52; Gaps 11;

OY 34 MIIDNK-VYDVREFFVDHGGGVILTHVKGDKGVDVDFTHPEAAW----- 77


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Db 124 LKANHVFLLYLHLILLDGAAMLTWEG--TSFLPFLCAVLLSAVOAQGMLOHDFG 182
OY 176 HHQVDFDRFGDLFGAFGLGVCOGSSWMKKDKNTHHAAPVNGEDPIDITPLTNS 235
Db 183 HLSVFSTSKMNLHNFVIGHLKGAPASWMNHMFQHNKPCFRKDPDINNHPF---- 238
OY 236 HALEMSDVPDEELTRMWSRFVYLNQTFYF-----PILSFARLSWCLQSLIFLPLNGOA 290
Db 239 FALGKILSY---ELGKQKKKMPYHNQHKYFFLIGRPALLPLFYQYI--FTFV----- 287
OY 291 HKPSGARVPISLVEQLSLAMHTWYLATMFLFKDPV-----NMLYFVLSQAVCNLLAI 346
Db 288 -----IQKKKWDLAAMITFVRFLLTYV--PLGLKAFGLGFLVRFLESNMFY 336
OY 347 VPSLNHNGRPVSKPEAVMDFFTKOITIGROVHGLFANMFLPGANGYOEIHHLPSPMR 406
Db 337 VQOMNIIPMHI---DHDRNMDVSTOLQATCNVHKSAFNDWFSGLNFOIEHHLFPTMPR 393
OY 407 HNEFKIQAVERFLCKKYNRYHTTGMIETAEVFSRLNE 445
Db 394 HNHKVAPLVQSLCAKHGIEYQSKPLLSAFADIHSLE 432

RESULT 15
O60427 PRELIMINARY: PRT: 444 AA.
AC 060427:
DT 01-AUG-1998 (TREMblrel. 07, Created)
DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE BC269730_2 (HYPOTHEtical 52.0 KDA PROTEIN) (FATTY ACID DESATURASE 1).
GN DKFPP762M2311 OR FADS1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId:9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Coleman M., Skowronski E., Adamson A.W.,
RA Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Gaines J.,
RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA Liu S., Altix C., Andreise T., Trankheim M., Amico-Keller G.,
RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA Krommiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
RA Kobayashi A., Olsen A.S., Carrano A.V.;
RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-MELANOMA (MEMO CELL LINE);
RA Blum H., Bauersachs S., Mewes H.W., Well B., Wiemann S.;
RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-20318619; PubMed-1086062;
RA Marguardt A., Stohr H., White K., Weber B.H.F.;
RT "cDNA cloning, genomic structure, and chromosomal localization of
RT three members of the human fatty acid desaturase family.";
RL Genomics 66:175-183(2000).
CC -1 SIMILARITY: TO CYTOCHROME B5 DOMAIN.
DR EMBL; AC004770; AAC23397.1; -.
DR EMBL; AL512760; CAC21679.1; -.
DR EMBL; AF084558; AAC23120.1; -.
DR HSSP; P04166; IBSX.
DR InterPro; IPR001199; -.
DR Pfam; PF00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROME_B5.
DR PROSITE; PSS0255; CYTOCHROME_B5_2; 1.
SQ SEQUENCE 444 AA; 51964 MW; CC3C28D82A4A9BF2 CRC64;

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Query Match 21.2%; Score 523.5; DB 4; Length 444;
Best Local Similarity 30.1%; Pred. No. 1,1e-39;
Matches 138; Conservative 72; Mismatches 196; Indels 53; Gaps 13;

OY 2 AAAPSVRTTTRAVLNLAELNKGKDAEAPFLMITDNKYDVRFPDPPGSSVILTH-V 60
Db 12 AAGPPRPRTTWEEVAORSCGEER-----MLVIDRKYYNISEFRRRPGGSRVISHYA 63
OY 61 GKDGTVDFPTFHPDEAM--ETLANFVYVDI---DESDRIKNDDEFAEVRKLTLPQSG 115
Db 64 GQDAIDPFYAFHNKGLVKKYMNLSLIGELSPQSPSEFTKKELTDEFELRATYERNG 123
OY 116 YDSSKAYYAFKVSFNLICWGLSTVIAKQSTSLANVLSAALLGLFWQCGMLANDEL 175
Db 124 LKANHVFLLYLHLILLDGAAMLTWEG--TSFLPFLCAVLLSAVOAQGMLOHDFG 182
OY 176 HHQVDFDRFGDLFGAFGLGVCOGSSWMKKDKNTHHAAPVNGEDPIDITPLTNS 235
Db 183 HLSVFSTSKMNLHNFVIGHLKGAPASWMNHMFQHNKPCFRKDPDINNHPF---- 238
OY 236 HALEMSDVPDEELTRMWSRFVYLNQTFYF-----PILSFARLSWCLQSLIFLPLNGOA 290
Db 239 FALGKILSY---ELGKQKKKMPYHNQHKYFFLIGRPALLPLFYQYI--FTFV----- 287
OY 291 HKPSGARVPISLVEQLSLAMHTWYLATMFLFKDPV-----NMLYFVLSQAVCNLLAI 346
Db 288 -----IQKKKWDLAAMITFVRFLLTYV--PLGLKAFGLGFLVRFLESNMFY 336
OY 347 VPSLNHNGRPVSKPEAVMDFFTKOITIGROVHGLFANMFLPGANGYOEIHHLPSPMR 406
Db 337 VQOMNIIPMHI---DHDRNMDVSTOLQATCNVHKSAFNDWFSGLNFOIEHHLFPTMPR 393
OY 407 HNEFKIQAVERFLCKKYNRYHTTGMIETAEVFSRLNE 445
Db 394 HNHKVAPLVQSLCAKHGIEYQSKPLLSAFADIHSLE 432

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Search completed: August 9, 2001, 20:36:14
Job time: 713 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 9, 2001, 20:25:11 ; Search time 28.86 Seconds

(without alignments)
542.438 Million cell updates/sec

Title: US-09-367-013b-2

Perfect score: 2465
Sequence: 1 MAAPSVRTFTRAEVLNAEA.....EVFSRLNEVSKASKMGKRAQ 457

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	210.5	8.5	359	1	Q08871 synechocyst
2	157	6.4	132	1	CYB5_BOROF
3	153	6.2	135	1	CYB5_TOBAC
4	150	6.1	136	1	CYB5_TOBAC
5	143	5.8	134	1	CYB5_ARATH
6	143	5.8	134	1	CYB5_BRAOL
7	139	5.6	137	1	CYB5_ORISA
8	138	5.6	134	1	CYB5_ARATH
9	136	5.5	146	1	CYB5_RAT
10	135.5	5.5	120	1	CYB5_YEAST
11	135.5	5.5	120	1	NIA_CHLVU
12	130	5.3	134	1	CYB5_MUSDO
13	128.5	5.2	134	1	CYB5_HUMAN
14	127	5.2	146	1	CYB5_HUMAN
15	125	5.1	135	1	CYB5_CUSRE
16	125	5.1	147	1	FD3C_SESIN
17	123.5	5.0	909	1	NIA_PETMY
18	123.5	5.0	904	1	NIA_TOBAC
19	122.5	5.0	904	1	NIA_TOBAC
20	122.5	5.0	912	1	NIA_TOBAC
21	122.5	5.0	915	1	NIA_TOBAC
22	121	4.9	414	1	CYBR_DROME
23	121	4.9	443	1	FD6C_BRANA
24	121	4.9	621	1	NIA_MAIZE
25	119.5	4.8	133	1	CYB5_HORSE
26	118.5	4.8	918	1	NIA_CUCMA
27	118.5	4.8	864	1	NIA_VOLCA
28	117.5	4.8	900	1	NIA_LOTJA
29	117.5	4.8	917	1	NIA_ARATH
30	117	4.7	917	1	NIA_ARATH
31	117	4.7	920	1	NIA_CICIN
32	116.5	4.7	889	1	NIA_MAIZE
33	116.5	4.7	916	1	NIA_ORYSA

34	116	4.7	902	1	NIA_PHTIN	P39864 phycophthor
35	115.5	4.7	133	1	CYB5_HUMAN	P00167 homo sapien
36	115.5	4.7	881	1	NIA1_PHAVU	P39865 phaseolus v
37	114.5	4.6	133	1	CYB5_RABIT	P00169 oryctolagus
38	114.5	4.6	435	1	FD3D_ARATH	P48622 arabidopsis
39	114	4.6	383	1	FD3J_BRANA	P48624 brassica na
40	114	4.6	890	1	NIA1_PHAVU	P39866 phaseolus v
41	113.5	4.6	898	1	NIA1_PETMY	P27783 betula verr
42	113.5	4.6	911	1	NIA_LYCES	P17570 lycopersico
43	113.5	4.6	926	1	NIA_SPIOLO	P23312 spinacia ol
44	113	4.6	383	1	FD6E_ARATH	P46313 arabidopsis
45	112.5	4.6	905	1	NIA_FUSOX	P39863 fusarium ox

ALIGNMENTS

```

RESULT 1
ID      L1CD_SVNY3      STANDARD;      PRT;      359 AA.
AC      008871:
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DE      L1NOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESATURASE).
DE      DES6 OR SLD0262.
OS      Synechocystis sp. (strain PCC 6803).
OC      Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX      NCBI_TaxID=1148;
RN      [1]
RP      MEDLINE=93283633; PubMed=8389613;
RA      Reddy A.S., Nuccio M.L., Gross L.M., Thomas T.L.;
RT      "Isolation of a delta-6-desaturase gene from the cyanobacterium
RT      Synechocystis sp. strain PCC 6803 by gain-of-function expression in
RT      Arabidopsis sp. strain PCC 7120."
RL      Plant Mol. Biol. 22:293-300(1993).
RN      [2]
RP      MEDLINE=97061201; PubMed=8905231;
RA      Kaneke T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA      Miyajima N., Hirosewa M., Sugita M., Sasamoto S., Kimura T.,
RA      Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA      Okumura S., Shimo S., Takeuchi C., Wada T., Watanabe A.,
RA      Yamada M., Yasuda M., Tabata S.;
RT      "Sequence analysis of the genome of the unicellular cyanobacterium
RT      Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT      entire genome and assignment of potential protein-coding regions."
CC      DNA Res. 3:109-136(1996).
CC      -1- CATALYTIC ACTIVITY: L1NOLEOYL-COA + AH(2) + O(2) -> GAMMA-
CC      L1NOLEOYL-COA + A + 2 H(2)O.
CC      -1- COFACTOR: IRON.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      the European Bioinformatics Institute. There are no restrictions on its
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; L11421; AAA27286.1; -
DR      EMBL; D90914; BAA18502.1; -
KW      Oxidoreductase; Iron;
SQ      SEQUENCE 359 AA; 41425 MW; 33FB165AEB98C05F CRC64;

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Query Match 8.5%; Score 210.5; DB 1; Length 359;
Best Local Similarity 25.7%; Pred. No. 4.3e-10;
Matches 83; Conservative 55; Mismatches 124; Indels 61; Gaps 16;

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DB 42 LKTLIIVLW-LFSAMAFVLPFVFPRLIG-----CMVLALALAFSNVGHANDHNAV 95
OY 180 FQORFGDLFGALGVCQCFSSMMKDKHN-TTHAAPNVHGDDPIDRPLITNSEHAL 238
DB 96 SSNPINRVLGMYDPV--GLSEFLMRYNHYHTYTNLGHVHEH-----GDGAY 146
OY 239 EMRSVDPEDELRTMMSRFWMLNQTWFYFPLISFARLSMCSQSLFVLPNGQAKRPS-GAR 297
DB 147 RM---SPEGHVIGY-RF-----QGFYMGVLYLFIPFYWFLDYVLYLNGKHYDHKIPRF 198
OY 298 VPSLVEOJSLAMHWTWYLATMFLTKDPV-NMLVYFLVSQAVCGMLAIVESLNNHNGMP 356
DB 199 QPELTLASLIGIKLLMLGVLGFLALGFSIPEVLIGASYVMYGYVCTIFMLAH----- 254
OY 357 VLSKEE-----AVDMEFTKOITGRDV---HPGLFANMFTGGLNYOIEHHLEPSM 404
DB 255 VLESTFELPPDGSGAIDDEMAICQIRITANFATNPN--FMNFCGLNHOVTHLHPNT 312
OY 405 PRHNFSKIOPAVETLCKKYVRY 427
DB 313 CHIHYPOLENLIKDVCOFGEVRY 335

RESULT 2
CYB5_BOROF STANDARD: PRT: 132 AA.
ID CYB5_BOROF 004354:
AC 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE CYTOCHROME B5.
OS Borage officinalis (Bourrache) (Borage).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC euasterids I incertae sedis; Boraginaceae; Borage.
OX NCBI_Taxid=13363;
RN 11]
RP SEQUENCE FROM N.A.
RX MEDLINE-97268723: PubMed-9108131;
RA Sayanova O., Smith M.A., Lapinskas P.A., Stobart K., Dobson G.,
RA Christie W.W., Shewry P.R., Napier J.A.;
RT "Expression of a borage desaturase cDNA containing an N-terminal
RT cytochrome b5 domain results in the accumulation of high levels of
RT delta6-desaturated fatty acids in transgenic tobacco.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
CC OXYGENASES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL: U79011: AAC49701.1; -.
DR HSSP: P00171: ICYO.
DR Mendel, 15843; Borof; 1218; 15843.
DR InterPro: IPR001199; -.
DR Pfam: PF00173; heme_1; 1.
DR PRINTS: PR00363; CYTOCHROME_B5.
DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KW Electron transport; Transmembrane; Heme; Microsome.
FT BINDING 37 37 HEME LIGAND (BY SIMILARITY).
FT BINDING 61 61 HEME LIGAND (BY SIMILARITY).
FT TRANSMEM 104 124 POTENTIAL.
SQ SEQUENCE 132 AA; 14556 MW; 96EF72A06F2E8C5B CRC64;

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Query Match 6.4%; Score 157; DB 1; Length 132;
Best Local Similarity 46.5%; Pred. No. 3.2e-06;
Matches 40; Conservative 10; Mismatches 26; Indels 10; Gaps 4;

OY 8 RTTFAEVLNAEALNKGKDAEAPFLMIIDNKYVDREPEVDPGSG-SVLTTHVGKGDND 66
DB 3 KITTLAEV-----AQHNSKDC-----WLIINGKYVDYTKFLDEHPPGSDVLLSATGKDATD 54

OY 67 VF-DTFHPEANMFTLANFVYGDIDES 91
DB 55 DFEIDGHSSSAKAMLEDDYVYGDIDS 80

RESULT 3
CYB5_TOBAC STANDARD: PRT: 135 AA.
ID CYB5_TOBAC P49099:
AC 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE CYTOCHROME B5, SEED ISOFORM.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Solanales; Solanaceae; Nicotiana.
OX NCBI_Taxid=4097;
RN 11]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. SAMSUN; TISSUE=Seed;
RX MEDLINE-96009039: PubMed-7580860;
RA Napier J.A., Smith M.A., Stobart A.K., Shewry P.R.;
RT "Isolation of a cDNA encoding a cytochrome b5 specifically expressed
RT in developing tobacco seeds.";
RL Planta 197:200-202(1995).
CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
CC OXYGENASES. MAY PLAY A KEY ROLE IN THE MODIFICATION BY
CC DESATURATION OF FATTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHICH IN
CC THE DEVELOPING SEED IS UTILIZED FOR MEMBRANE SYNTHESIS AND IN THE
CC DEVELOPMENTALLY REGULATED PRODUCTION OF LARGE AMOUNTS OF STORAGE
CC LIPIDS.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING SEEDS.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL: X80008; CA56318.1; -.
DR HSSP: P00171; IWD8.
DR InterPro: IPR001199; -.
DR Pfam: PF00173; heme_1; 1.
DR PRINTS: PR00363; CYTOCHROME_B5.
DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KW Electron transport; Transmembrane; Heme; Microsome; Multigene family.
FT BINDING 40 40 HEME LIGAND (BY SIMILARITY).
FT BINDING 64 64 HEME LIGAND (BY SIMILARITY).
FT TRANSMEM 107 127 POTENTIAL.
SQ SEQUENCE 135 AA; 14869 MW; A36CCA081A72EBCB CRC64;

Query Match 6.2%; Score 153; DB 1; Length 135;
Best Local Similarity 45.3%; Pred. No. 7.1e-06;
Matches 39; Conservative 10; Mismatches 27; Indels 10; Gaps 4;

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QY 8 RTFTAAEVLNMEALNEGGKKDAAPFLMIIDNNVYVUREVPDH-
CGSVILTHVGGDGD 66
Db 6 KVFETLAEVSN-----HNNAKDC-----WLIISGAVYNTKRLBDHPGGGEVLLSATGDAID 57
QY 67 VF-DTFPEAMETLANFYGVGIDSS 91
Db 58 DFEDIGHSSSARAMEIDFYGVGIDSS 83

RESULT 4

AD	CYB5_TOBAC	STANDARD;	PRT;	136 AA.
AC	P49098;			
DT	01-FEB-1996	(Rel. 33, Created)		
DT	01-FEB-1996	(Rel. 33, Last sequence update)		
DT	01-OCT-2000	(Rel. 40, Last annotation update)		
DE	CYTOCHROME B5.			
OS	Nicotiana tabacum (Common tobacco).			
CC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;			
CC	Magnoliophyta; Eudicotyledons; Core eudicots; Asteridae; euasterids I;			
CC	Solanales; Solanaceae; Nicotiana.			
OX	NCBI_TaxID=4097;			
RN	[1]			
RP	SEQUENCE FROM N.A.			

RA Smith M.A., Stobart A.R., Sherry P.R., Napier J.A. ;
RT "tobacco cytochrome b5: cbna isolation, expression analysis and in
RT vitro protein targeting".
RL Plant Mol. Biol. 25:527-537 (1994).
CC -I- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
CC OXYGENASES. MAY PLAY A KEY ROLE IN THE MODIFICATION BY
CC DESATURATION OF FATTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHICH IN
CC THE DEVELOPING SEED IS UTILIZED FOR MEMBRANE SYNTHESIS AND IN THE
CC DEVELOPMENTALLY REGULATED PRODUCTION OF LARGE AMOUNTS OF STORAGE
CC LIPIDS. IS INVOLVED IN THE REDUCTION OF CYTOCHROME P-450 AND
CC MAY THEREFORE BE INVOLVED IN FLAVONOID BIOSYNTHESIS IN THE PETALS.
CC -I- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -I- TISSUE SPECIFICITY: IS HIGHLY EXPRESSED IN DEVELOPING SEEDS,
CC MODERATELY EXPRESSED IN FLOWERS, AND IS EXPRESSED AT LOW
CC LEVELS IN THE LEAF.
CC -I- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC -----
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DR	EMBL: X71441:	CAA50575.1	ALT_INIT.
DR	EMBL: X68140:	CAA48240.1	-
DR	HSSP: P04166:	1B5M.	
DR	InterPro: IPR001199:	-	
DR	pfam: PF001173:	heme_1	1.
DR	PRINTS: PR00363:	CYTCHROME.B5.	
DR	PROSITE: PS00191:	CYTCHROME_B5_1	1.
DR	PROSITE: PS50255:	CYTCHROME_B5_2	1.
KW	Electron transport:	Transmembrane	Heme: Microsome: Multigene family.
FT	BINDING	40	40
FT	BINDING	64	64
FT	TRANSMEM	107	127
FT	CONFLICT	10	11
FT	CONFLICT	105	105
SQ	SEQUENCE	136 AA:	14979 MW: DACE9EA695B2835F CXC64;

Query Match	6.18;	Score 150;	DB 1;	Length 136;
Best Local Similarity	43.08;	Pred. NO. 1.3e-05;		

	Matches	37;	Conservative	12;	Mismatches	27;	Indels	10;	Gaps	4;
OY	8	RPTETAAYLNALAEKGKDAAPFLMIITDNKKAYDVDFREPPOPGS-STYLHHVGGTND	66	:		:		:		:
Db	6	KFTFLAEEV-----SQNNKKDC-----WLVSGKAVDYTKRLDDHPGDEVLLSATCGDARD	57	:		:		:		:
OY	67	VF-DTFHPEAMETLANFYGDIDES	91	:		:		:		:
Db	58	DDEDVGHSARAMLDEIYIGIDSA	83	:		:		:		:

RESULT

ID	CY52_ARATH	STANDARD;	PRT;	134 AA.
AC	048845;			
DT	01-OCT-2000	(Rel. 40, Created)		
DT	01-OCT-2000	(Rel. 40, Last sequence update)		
DT	01-OCT-2000	(Rel. 40, Last annotation update)		
DE	PROBABLE CYTOCHROME B5 ISOFORM 2.			
GN	ATG32720 OR F24L7.14.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;			
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;			
OC	Brassicales; Brassicaceae; Arabidopsis.			
OX	NCBI_TaxID=3702;			

RC STRAIN-CV, COLUMBIA:
RX MEDLINE-20083487, PubMed-10617197:
RA Lin X., Keul S., Rounsley S.D., Stoe T.P., Benito M.-I., Town C.D.,
RA Fujii C.T., Mason T.M., Bowman C.L., Batnstead M.E., Feldlyum T.V.,
RA Buell C.R., Cechum K.A., Lee J.J., Rönning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., Vanaken S.E., Umeyam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carreira A.J., Cressy T.H., Goodman H.M., Somerville C.R.,
RA Copenhagen G.P., Pius D., Niernan W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.:
RT "Sequence and analysis of chromosome 2 of the plant *Arabidopsis*
RT *thaliana*.";
RL Nature 402:761-768(1999).
CC -i- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
CC OXYGENASES (BY SIMILARITY).
CC -i- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE, BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -i- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).

DR EMBL: AC003974; AAC04491.1; -.
DR HSP; P04166; 1B5M.
DR Mendel; 27943; Arab; 1218; 27943.
DR InterPro: IPR001199; -.
DR Pfam: PF00173; heme_1; 1.
DR PRINTS: PR00363; CYTOCHROMEB5.
DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KW Electron transport; Transmembrane; Heme; Microsome; Multigene family.
FT BINDING 40 HEME LIGAND (BY SIMILARITY).
FT BINDING 64 HEME LIGAND (BY SIMILARITY).
FT TRANSMEM 107 127 POTENTIAL.
SQ SEQUENCE 134 AA; 15016 MW; B405F5430F5716C1 CRC64;

Query Match	5.8%	Score 143	DB 1	Length 134
Best Local Similarity	50.0%	Pred No. 4.7e-05		
Matches 29	Conservative 12	Mismatches 15	Indels 2	Gaps 2

QY 34 MIDNKVYDVRFPDHPGG-SVILTHVGKDGDFV-DTFHPEAMETLANFYVGDI 89
 DB 24 IYINGKVVVTFLEBDHPGGDVLISSTGKDATDDEFEDVGHSHSASAKEMEQYVVGID 81

RESULT 6
 ID CYB5_BRAOL STANDARD; PRT; 134 AA.
 AC P40934;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CYTOCHROME B5.
 GN CYB5.
 OS Brassica oleracea (Cauliflower).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Brassica.
 OC NCBI_TaxID=3712;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 6-47 AND 75-89.
 RC STRAIN=CV. CAULIFLORA.
 RA Keans E.V., Neck P., Somerville C.R.;
 RT "Nucleotide sequence of cDNA for cytochrome b5 from cauliflower
 (Brassica oleracea L.)."
 RL Plant Physiol. 99:1254-1257(1992).
 CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
 CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
 CC OXYGENASES.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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 CC -----
 CC EMBL: M87514; AAA32990.1; -
 CC HSSP: P00171; 3B5C.
 CC InterPro: IPR001199; -
 CC Pfam: PF00173; heme_1; 1.
 CC PRINTS: PR00363; CYTOCHROME_B5.
 CC PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 CC PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 CC Electron transport; Transmembrane; Heme; Microsome.
 CC FT BINDING 40 40 HEME LIGAND (BY SIMILARITY).
 CC FT BINDING 64 64 HEME LIGAND (BY SIMILARITY).
 CC TRANSMEM 107 127 POTENTIAL.
 CC FT VARIANT 5 5 K -> N.
 CC SEQUENCE 134 AA; 15062 MW; 764DC24A4CDD591 CRC64;

Query Match 5.8%; Score 143; DB 1; Length 134;
 Best Local Similarity 40.0%; Pred. No. 4.7e-05;
 Matches 32; Conservative 16; Mismatches 28; Indels 4; Gaps 3;

QY 14 EVLNAEALNEGGKDAEPFLMIIDNKVYDVRFPDHPGG-SVILTHVGKDGDFV-DTF 71
 DB 6 KVLGFEVSOHNKTKDC--WLISGKVVYDTPMDHDPGGDVLISSTGKDANDEPDVG 63
 QY 72 HPEANETLANFYVGDI 91
 DB 64 HSDTARDMEKYYIGEDIS 83

RESULT 7
 ID CYB5_ORYSA STANDARD; PRT; 137 AA.
 AC P49100;

DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CYTOCHROME B5.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae;
 OC Oryza.
 OC NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Callus;
 RX MEDLINE=94325476; PubMed=8049375;
 RA Smith M.A., Stobart A.K., Shewry P.R., Napier J.A.;
 RT "Tobacco cytochrome b5: cDNA isolation, expression analysis and in
 RT vitro protein targeting."
 RL Plant Mol. Biol. 25:527-537(1994).
 CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
 CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
 CC OXYGENASES.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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 CC -----
 CC EMBL: X75670; CA53366.1; -
 CC HSSP: P00171; 3B5C.
 CC InterPro: IPR001199; -
 CC Pfam: PF00173; heme_1; 1.
 CC PRINTS: PR00363; CYTOCHROME_B5.
 CC PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 CC PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 CC Electron transport; Transmembrane; Heme; Microsome.
 CC FT BINDING 41 41 HEME LIGAND (BY SIMILARITY).
 CC FT BINDING 65 65 HEME LIGAND (BY SIMILARITY).
 CC TRANSMEM 108 128 POTENTIAL.
 CC SEQUENCE 137 AA; 15296 MW; 4260C9D633E0FDA CRC64;

Query Match 5.6%; Score 139; DB 1; Length 137;
 Best Local Similarity 41.9%; Pred. No. 0.0001;
 Matches 36; Conservative 11; Mismatches 29; Indels 10; Gaps 4;

QY 8 RFTTRAEVNAEALNEGGKDAEPFLMIIDNKVYDVRFPDHPGG-SVILTHVGKDGTD 66
 DB 7 KYITLLEEV-----AKHNSKDC---WLISGKVVYNSKLEBDHPGGDVLISSTGKDARD 58

QY 67 VF-DTFHPEANETLANFYVGDI 91
 DB 59 DREDVGHHTTARAMDEYYVGDIDTS 84

RESULT 8
 ID CY51_ARATH STANDARD; PRT; 134 AA.
 AC 042342; O9SB05;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CYTOCHROME B5 ISOFORM 1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]

```

RP SEQUENCE FROM N.A.
RP STRAIN-CV. COLUMBIA;
RX PubMed-9880378;
RA Fukuchi-Mizutani M., Mizutani M., Tanaka Y., Kusumi T., Ohta D.;
RT "Mitochondrial electron transfer in higher plants: cloning and
RT heterologous expression of NADH-cytochrome b6/f reductase from
RT Arabidopsis.";
RL Plant Physiol. 119:353-361(1999).
RN [2]
RP SEQUENCE OF 1-113 FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA Cooke R., Laudie M., Raynal M., Delzeny M.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
CC OXYGENASES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE, BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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CC -----
DR EMBL; AB007801; CAB17231.1; -.
DR EMBL; F20001; CAA2337.1; -.
DR Mendel; 6696; Arath.1218; 6696.
DR HSP; P00171; ICYO.
DR InterPro; IPR001199; -.
DR Pfam; PF00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROME_B5.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Electron transport; Transmembrane; Heme; Microsome; Multigene family.
FT BINDING 40 40 HEME LIGAND (BY SIMILARITY).
FT BINDING 64 64 HEME LIGAND (BY SIMILARITY).
FT TRANSMEM 107 127 POTENTIAL.
FT CONFLICT 1 3 MSS -> ARA (IN REF. 2).
SQ SEQUENCE 134 AA; 15084 MW; 9EC01C60F7C873FD CXC64;

Query Match 5.6%; Score 138; DB 1; Length 134;
Best Local Similarity 38.8%; Pred. No. 0.00012;
Matches 31; Conservative 18; Mismatches 27; Indels 4; Gaps 3;

OY 14 EVLNAEALNECKKDAEAPFLMIIDNKYYDREFPVDHGG-SVILTGWGKGDTDF-DTF 71
   ||| : :: | : :|| ||||| : :||| : :||| : :||| : :||| : :|||
Db 6 KVLSEFEESKINKTKDC--WLISGKYVDVPFMDDHGDEVLSTSGKDATNDFDVG 63
OY 72 HPEAMETLANFYGVGDIDDS 91
Db 64 HSDTARDMDKFTGEIDSS 83

RESULT 9
CYMS_RAT STANDARD; PRT; 146 AA.
AC P04165; Q9QWGI;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CYTOCHROME B5 OUTER MITOCHONDRIAL MEMBRANE ISOFORM PRECURSOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
NN [1]
RP SEQUENCE FROM N.A.
```

```

RA Kurudo R., Ikenoue T., Honsho M., Tujimoto S., Mirima Y., Ito A.;
RT "charged amino acids at the carboxy-terminal portions determine
RL intracellular locations of two isoforms of cytochrome b5.";
RN Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RP
RX MEDLINE=83182449; Pubmed=6840088;
RA Lederer F., Chir R., Guillard B., Cortial S., Ito A.;
RT "Two homologous cytochromes b5 in a single cell.";
RL Eur. J. Biochem. 132:95-102(1983).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=97128656; Pubmed=8973214;
RA Rodriguez-Meranon M.J., Qiu F., Stark R.E., White S.P., Zhang X.,
RA Foundling S.I., Rodriguez V., Schilling C.L. III, Bunce R.A.;
RT "13C NMR spectroscopic and x-ray crystallographic study of the role
RL played by mitochondrial cytochrome b5 heme propionates in the
RL electrostatic binding to cytochrome c.";
RL Biochemistry 35:16378-16390(1996).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=98145212; Pubmed=9484218;
RA Rivera M., Seetharaman R., Girdhar D., Wirtz M., Zhang X., Wang X.,
RA White S.;
RT "The reduction potential of cytochrome b5 is modulated by its exposed
RT heme edge.";
RL Biochemistry 37:1485-1494(1998).
CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
CC OXYGENASES.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL OUTER MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC -----
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CC -----
DR EMBL: Y12517; CAAT73117.1; -.
DR PIR: A00173; CBRT5M.
DR PDB: 1B5M; 12-MAR-97.
DR PDB: 1AWP; 18-NOV-98.
DR InterPro: IPR001199; -.
DR Pfam: PF00173; heme_1; 1.
DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE: PS50253; CYTOCHROME_B5_2; 1.
KW Electron transport; Mitochondrion; Outer membrane; Transmembrane;
KW Heme; 3D-structure.
FT FT PROPEP 1 11
FT FT CHAIN 12 146 CYTOCHROME B5 OUTER MITOCHONDRIAL
FT FT DOMAIN 12 103 MEMBRANE ISOFORM.
FT FT TRANSMEM 119 136 HEME-BINDING.
FT FT BINDING 55 55 HEME LIGAND (BY SIMILARITY).
FT FT BINDING 79 79 HEME LIGAND (BY SIMILARITY).
FT FT CONFLICT 12 12 N -> D (IN REF. 2).
SQ SEQUENCE 146 AA; 16265 MW; 1CA90DD3C81C412B CRC64;
Query Match 5.5%; Score 136; DB 1; Length 146;
Best Local Similarity 24.6%; Pred. No. 0.0002;
Matches 46; Conservative 22; Mismatches 53; Indels 66; Gaps 9;
QY 5 PSVRTFTAEVYLNALNEGRKDAEAPLMTIDNKVYDFEVPDPHGCG-SVILTNGKD 63
Dy 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1
18 PAVTYRILEEV-----AKRNTAEETWVYIGHGVYDITRFLSEHPGGEVILDEAGD 69
Gy 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1
64 GTDVF-DTFHEEAMETLANFYVGDIIDSDRDIKNDPEAAEYVKRLRTLFQSLGTYDSSKA 122
1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1

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Db 70 ATESEEDVGHSPDAREMLKQYIGDHPNDLPRKGD-----KDPKRN 112
QY 123 YAFVSENLG--IWGLSVIVAKNGQSTLANVLASALLGLEWQCGSLADFLHOFV 180
Db 113 -----NSCQSSW-----AYW-----IVPIVGALLIGFLYR----- 137
QY 181 QDRFMGD 187
Db 138 --HFVMD 142

RESULT 10
CYB5_YEAST STANDARD: PRT: 120 AA.
AC P4012:
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CYTOCHROME B5.
GN CYB5 OR YNL11C OR N1949.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OC NCBI_TaxID=4932;
RN NCB1
RP SEQUENCE FROM N.A.
RC STRAIN=FL100;
RX MEDLINE=94237477; PubMed=8181746;
RA "Truan G., Eplinat J.-C., Rougeulle C., Cullin C., Pompon D.;
RT "Cloning and characterization of a yeast cytochrome b5-encoding gene
RT which suppresses ketoconazole hypersensitivity in a NADPH-P-450
RT reductase-deficient strain."
RL Gene 142:123-127(1994).
RN NCB1
RP SEQUENCE FROM N.A.
RX MEDLINE=97245296; PubMed=9090055;
RA de Antoni A., D'Angelo M., Dal Pero F., Sartorello F., Pandolfo D.,
RA Pallavicini A., Lanfranchi G., Valle G.;
RT "The DNA sequence of cosmid 14-13b from chromosome XIV of
RT Saccharomyces cerevisiae reveals an unusually high number of
RT overlapping open reading frames."
RL Yeast 13:261-266(1997).
CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CC OXIDASES. IT PLAYS A ROLE IN FATTY-ACID DESATURATION AND IS ALSO
CC INVOLVED IN SEVERAL STEPS OF THE STEROL BIOSYNTHESIS PATHWAY,
CC PARTICULARLY IN THE 4'-DEMETHYLATION OF THE 4',4'-DIMETHYL
CC ZYMOSTEROL.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE. BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L22494; AAA67468.1; -
CC EMBL: Z69382; CAA93396.1; -
CC EMBL: Z71387; CAA95990.1; -
CC PIR: S47919; S47919.
CC HSSP: P04166; 1B5M.
CC SGP: S0005055; CYB5.
CC InterPro: IPR001199; -
CC Pfam: PF00173; heme_1; 1.
CC PRINTS: PS00363; CYTOCHROME_B5.
CC PROSITE: PS00191; CYTOCHROME_B5_1; 1.
CC PROSITE: PS50255; CYTOCHROME_B5_2; 1.
CC Electron transport; Transmembrane; Heme; Mitochondrion;
CC BINDING 37 37 HEME LIGAND (BY SIMILARITY).

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FT BINDING 61 61 HEME LIGAND (BY SIMILARITY).
FT TRANSMEM 98 118 POTENTIAL.
FT CONFLICT 17 17 E -> O (IN REF. 1).
SQ SEQUENCE 120 AA: 13297 MW: 59682A6730CAD19 CRC64:

Query Match
Best Local Similarity 33.7%; Score 135.5; DB 1; Length 120;
Matches 33; Conservative 18; Mismatches 42; Indels 5; Gaps 3;

QY 32 FLMIIDNKVYDVEFPYDPHGGSVILTHV-GKGDVDF-DTFHPENAMETLANFYGDID 89
Db 19 FWIIIDDKYDVDSQFDEHGDDEIIMDGODATESFYDIGHSDRLRLKGLYIGDVD 78
QY 90 ESDROIKNDDFAEVRKLR---TLFQSLGYSSKAY 124
Db 79 KTSERYSVKSTSENQSGSTLVVITAILMGVAAY 116

RESULT 11
NIA_CHLVU STANDARD: PRT: 318 AA.
AC Q01170;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE NITRATE REDUCTASE (EC 1.6.6.1) (NR) (FRAGMENT).
DE Chlorobacterium vulgare.
OS Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorobiales;
OC Chlorobacteriales; Chlorobacteriaceae; Chlorobacter.
OC NCB1_TaxID=3077;
RN NCB1
RP SEQUENCE FROM N.A.
RX MEDLINE=91354204; PubMed=1883330;
RA Cannons A.C., Iida N., Solomonson L.P.;
RT "Expression of a cDNA clone encoding the haem-binding domain of
RT Chlorobacterium nitrate reductase."
RL Biochem. J. 278:203-209(1991).
CC -1- FUNCTION: NITRATE REDUCTASE IS A KEY ENZYME INVOLVED IN THE FIRST
CC STEP OF NITRATE ASSIMILATION IN PLANTS, FUNGI AND BACTERIA.
CC -1- CATALYTIC ACTIVITY: NADH + NITRATE = NAD(+) + NITRITE + H(2)O.
CC -1- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,
CC HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
CC GROUP IS CALLED CYTOCHROME B-557.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: CONTAINS A CYTOCHROME B5 FAMILY, HEME-BINDING DOMAIN.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC -----
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CC -----
CC EMBL: X56771; CAA40090.1; -
CC PIR: S17197; S17197.
CC HSSP: P04166; 1B5M.
CC InterPro: IPR000572; -
CC InterPro: IPR001199; -
CC Pfam: PF00173; heme_1; 1.
CC Pfam: PF00174; oxidored_molyb_1.
CC PROSITE: PS00191; CYTOCHROME_B5_1; 1.
CC PROSITE: PS50255; CYTOCHROME_B5_2; 1.
CC DR PROSITE: PS00559; MOLYBDOPTERIN_EUK; PARTIAL.
CC Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
CC Nitrate assimilation.
CC NON_TER 1 1
CC BINDING 251 251 HEME LIGAND (BY SIMILARITY).

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FT BINDING 274 274 HEME LIGAND (BY SIMILARITY).
NON_TER 318 318
SO SEQUENCE 318 AA: 34830 MW: E60D82FE1E98292A CRC64:

Query Match 5.58; Score 135.5; DB 1; Length 318;
Best Local Similarity 34.08; Pred. No. 0.00056;
Matches 34; Conservative 16; Mismatches 41; Indels 9; Gaps 3;

QY 3 AASVRFETRAEVLNAALENGKKADEAPFLMIDNKVYDVREFVPHPGS-VILTHVG 61
DB 212 APGANSFTAAEV-----ETHTTMSAW-EYVDGKYDTPTPKDHPGASDILLVAG 263
QY 62 KDGTDFEFTFHPPEAMETLANFYVDIDESDRIDKNDFA 101
DB 264 IDATDEFNAIHSLLKAKQKLEIYIGELAEFGQEAASDRA 303

RESULT 12

CYB5_MUSDO STANDARD; PRT; 134 AA.
ID CYB5_MUSDO
AC P49096;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CYTOCHROME B5 (CYTB5).
OS Musca domestica (House fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Muscoidae; Muscidae; Musca.
NCBI_TaxID=7370;
RN 1)
RP SEQUENCE FROM N.A.
RC STRAIN=ROTTERS;
RA Guzey V., Feyereisen R.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
OXYGENASES.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE. BOUND TO THE
CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L38464; AAA56985.1; -
CC HSSP: P04166; IBSM;
DR InterPro: IPR001199; -
DR Pfam: PF00173; heme_1; 1.
DR PRINTS: PR00363; CYTOCHROME_B5.
DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE: PS00255; CYTOCHROME_B5_2; 1.
KW Electron transport; Transmembrane; Heme; Mitochondrion.
FT BINDING 41 41
FT BINDING 65 65 HEME LIGAND (BY SIMILARITY).
FT TRANSMEM 111 131
FT POTENTIAL.
SO SEQUENCE 134 AA: 15401 MW: 11A1A23E235EC3AA CRC64:

Query Match 5.38; Score 130; DB 1; Length 134;
Best Local Similarity 35.5%; Pred. No. 0.00055;
Matches 33; Conservative 15; Mismatches 35; Indels 10; Gaps 3;

QY 3 AASVRFETRAEVLNAALENGKKADEAPFLMIDNKVYDVREFVPHPGS-VILTHVG 61
DB 2 SSEDVKTFTAAEV-----AKNNTDKMFWIITHNNVDTAFLANHPGGEVLLIDGAG 53

QY 62 KDGTDFEFTFHPPEAMETLANFYVDIDESDR 93
DB 54 KDTEHFEDVGHSSDAREMKQYKVGELVAER 86

Query Match 5.58; Score 135.5; DB 1; Length 318;
Best Local Similarity 34.08; Pred. No. 0.00056;
Matches 34; Conservative 16; Mismatches 41; Indels 9; Gaps 3;

QY 3 AASVRFETRAEVLNAALENGKKADEAPFLMIDNKVYDVREFVPHPGS-VILTHVG 61
DB 212 APGANSFTAAEV-----ETHTTMSAW-EYVDGKYDTPTPKDHPGASDILLVAG 263
QY 62 KDGTDFEFTFHPPEAMETLANFYVDIDESDRIDKNDFA 101
DB 264 IDATDEFNAIHSLLKAKQKLEIYIGELAEFGQEAASDRA 303

RESULT 13

CYB2_HANAN STANDARD; PRT; 573 AA.
ID CYB2_HANAN
AC P09437;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CYTOCHROME B2 PRECURSOR (EC 1.1.2.3) (L-LACTATE DEHYDROGENASE
[CYTOCHROME]) (L-LACTATE FERRICYTOCHROME C OXIDOREDUCTASE) (L-LCR).
GN CYB2.
OS Hansenula anomala (Yeast) (Candida pelliculosa).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
NCBI_TaxID=4927;
RN 1)
RP SEQUENCE FROM N.A.
RX MEDLINE=90045973; PubMed=2813072;
RA Ristler Y., Tegoni M., Gervais M.;
RT "Nucleotide sequence of the Hansenula anomala gene encoding
RT flavocytochrome b2 (L-lactate:cytochrome c oxidoreductase).";
RL Nucleic Acids Res. 17:8381-8381(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90088451; PubMed=2688640;
RA Black M.T., Gunn F.J., Chapman S.K., Reid G.A.;
RT "Structural basis for the kinetic differences between
RT flavocytochromes b2 from the yeasts Hansenula anomala and
RT Saccharomyces cerevisiae.";
RL Biochem. J. 263:973-976(1989).
RN [3]
RP SEQUENCE OF 80-163.
RX MEDLINE=88082787; PubMed=3319613;
RA Hamont P.-Y., Thomas M.-A., Labeyrie F., Lederer F.;
RT "Amino acid sequence of the cytochrome-b5-like heme-binding domain
RT from Hansenula anomala flavocytochrome b2.";
RL Eur. J. Biochem. 169:539-546(1987).
CC -1- CATALYTIC ACTIVITY: L-LACTATE + 2 FERRICYTOCHROME C = PYRUVATE +
2 FERROCYTOCHROME C.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INTERMEMBRANE SPACE.
CC -1- MISCELLANEOUS: THIS ENZYME BINDS FMN AND PROTOHEME IX PROSTHETIC
GROUPS.
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
B5 FAMILY.
CC -1- SIMILARITY: TO SPINACH GLYOXALATE OXIDASE (33% IDENTITY), TO
P. PUTIDA S-MANDELATE DEHYDROGENASE, AND TO M. SNEGMATIS LACTATE
2-MONOOXYGENASE.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X16051; CAA34183.1; -
CC PIR: S06600; S06600.
DR HSSP: P00175; ILCO.
DR InterPro: IPR000262; -
DR InterPro: IPR001199; -
DR Pfam: PF01070; FMN_dh; 1.
DR Pfam: PF00173; heme_1; 1.
DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE: PS00255; CYTOCHROME_B5_2; 1.
DR PROSITE: PS00557; FMN_HYDROXYL_ACID_DH; 1.
KW Electron transport; Respiratory chain; Oxidoreductase; Flavoprotein;
FMN; Heme; Mitochondrion; Transit peptide.

FT TRANSIT 1 73 MITOCHONDRION.
 FT CHAIN 74 573 CYTOCHROME B2.
 FT DOMAIN 80 163 CYTOCHROME DOMAIN (CORE).
 FT BINDING 115 115 HEME LIGAND (BY SIMILARITY).
 FT BINDING 138 138 HEME LIGAND (BY SIMILARITY).
 FT ACT_SITE 432 432 REMOVES THE SUBSTRATE ALPHA-PROTON AS THE
 FT ACT_SITE 432 432 FIRST STEP IN CATALYSIS (BY SIMILARITY).
 FT ACT_SITE 435 435 SUBSTRATE BINDING (BY SIMILARITY).
 SQ SEQUENCE 573 AA; 64202 MW; 83EEF645C580BC8E CRC64;

Query Match 5.2%; Score 128.5; DB 1; Length 573;
 Best Local Similarity 24.7%; Pred. No. 0.0044; Matches 36; Conservative 32; Mismatches 41; Indels 37; Gaps 8;

OY 10 FTRAEEV-----LNAAEALNE-GKDAEAPFLMIIDNKYVDREFPDPHGG-SVILTHV 60
 DB 70 FIASADVPHMKDELTPETVISQHNKCD--DLWVYLVNGQYVLDLPFPHNGCGKIIIRRA 126
 OY 61 GKDGTVPDTPFPEAAWETLANE-----YGDIDESDRDKND--DFAAEVRKRLT 109
 DB 127 GKDATKIFVPIHP--DTIEKFIPEKHLGVLVEGEDEEELSDIEDRLERIERKPP 183
 OY 110 LFOSLGYPD-----SSKAYY 124
 DB 184 LSONMLHDFETIARQILPPALAYY 209

RESULT 14
 CYM5_HUMAN STANDARD; PRT; 146 AA.

AC 043169;
 DT 01-OCT-2000 (Rel. 40; Created)
 DT 01-OCT-2000 (Rel. 40; Last sequence update)
 DT 01-OCT-2000 (Rel. 40; Last annotation update)
 DE CYTOCHROME B5 OUTER MITOCHONDRIAL MEMBRANE ISOFORM PRECURSOR.
 GN OMB5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Ishibashi K.;
 RT "Cytochrome b5 and aquaporins share the last transmembrane amino acids
 sequence.";
 RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
 CC OXYGENASES (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL OUTER MEMBRANE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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 CC EMBL: AB009282; BAA23735.1; -
 DR HSSP: P04166; 1BSM.
 DR InterPro: IPR001199; -
 DR Pfam: PF00173; heme_L; 1.
 DR PRINTS: PR00363; CYTOCHROME B5.
 DR PROSITE: PS00191; CYTOCHROME B5_1; 1.
 DR PROSITE: PS50255; CYTOCHROME B5_2; 1.
 KW Electron transport; Mitochondrion; Outer membrane; Transmembrane;
 KW Heme
 FT PROPEP 1 11 BY SIMILARITY.

FT CHAIN 12 146 CYTOCHROME B5 OUTER MITOCHONDRIAL
 FT DOMAIN 12 103 MEMBRANE ISOFORM.
 FT TRANSMEM 119 136 HEME-BINDING.
 FT BINDING 55 55 HEME LIGAND (BY SIMILARITY).
 FT BINDING 79 79 HEME LIGAND (BY SIMILARITY).
 SQ SEQUENCE 146 AA; 16332 MW; 2FF7DBA29124E19 CRC64;

Query Match 5.2%; Score 127; DB 1; Length 146;
 Best Local Similarity 36.0%; Pred. No. 0.0011; Matches 32; Conservative 12; Mismatches 35; Indels 10; Gaps 3;

OY 6 SVRTFTRAEEVLNAAEALNECKDAEAPFLMIIDNKYVDREFPDPHGG-SVILTHV 64
 DB 19 SVYVYRLAEERAKNSLKE-----LWLVHGRVYDTRFLNEHGGVLELLEAGVDA 70
 OY 65 TDVF-DTPFPEAAWETLANEYVDIDESD 92
 DB 71 SESEFEDVGHSSDAREMLKQYIGDIHPSD 99

RESULT 15

CYB5_CUSRE STANDARD; PRT; 135 AA.

AC P49097;
 DT 01-FEB-1996 (Rel. 33; Created)
 DT 01-FEB-1996 (Rel. 33; Last sequence update)
 DT 01-OCT-2000 (Rel. 40; Last annotation update)
 DE CYTOCHROME B5.
 OS Cuscuta reflexa (Southern Asian dodder).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
 OC Solanales; Convolvulaceae; Cuscuta.
 OX NCBI_Taxid=4129;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=95047507; PubMed=7959021;
 RA Subramaniam K., Mahadevan S.;
 RT "The cdna sequence of cytochrome b5 associated with cytokinin-induced
 RT haustoria formation in Cuscuta reflexa.";
 RL Gene 149:375-376(1994).
 CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
 CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
 CC OXYGENASES.
 CC -1- SUBCELLULAR LOCATION: MICROSOmal MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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 CC or send an email to license@sib-sib.ch).
 CC EMBL: L22209; AAA62621.1; -
 DR HSSP: P04166; 1BSM.
 DR InterPro: IPR001199; -
 DR Pfam: PF00173; heme_L; 1.
 DR PRINTS: PR00363; CYTOCHROME B5.
 DR PROSITE: PS00191; CYTOCHROME B5_1; 1.
 DR PROSITE: PS50255; CYTOCHROME B5_2; 1.
 KW Electron transport; Transmembrane; Heme; Microsome.
 FT BINDING 39 39 HEME LIGAND (BY SIMILARITY).
 FT BINDING 63 63 HEME LIGAND (BY SIMILARITY).
 FT TRANSMEM 106 126 POTENTIAL.
 SQ SEQUENCE 135 AA; 14745 MW; CFP2IC952981P5DA CRC64;

Query Match 5.1%; Score 125; DB 1; Length 135;
 Best Local Similarity 46.7%; Pred. No. 0.0014;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 9, 2001, 20:22:01 ; Search time 50.69 Seconds

(without alignments)
686.758 Million cell updates/sec

Title: US-09-367-013b-2

Perfect score: 2465
Sequence: 1 MAAPSVRTFTRAEVLAAEA.....EVFSRLNEVSKAASKMGKQAQ 457

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	629	25.5	447	1 T43319	Delta5 fatty acid
2	537	21.8	473	1 T26280	linoleoyl-CoA desa
3	534.5	21.7	458	2 S68358	Delta8 sphingolip
4	522	21.2	449	2 T47950	delta-8 sphingolip
5	502	20.4	449	2 T50355	hypotheical prote
6	497.5	20.2	449	2 A84900	linoleoyl-CoA desa
7	460	18.7	444	2 T13155	Delta6 fatty acid
8	445.5	18.1	444	2 JG0180	linoleoyl-CoA desa
9	432	17.5	523	3 JC7556	linoleoyl-CoA desa
10	422.5	17.1	345	2 T36617	linoleoyl-CoA desa
11	227	9.2	368	2 S54809	linoleoyl-CoA desa
12	210.5	8.5	359	2 S35157	Delta6 fatty acid
13	173.5	7.0	370	2 B83034	conserved hypotet
14	169.5	6.9	427	2 G70590	probable desA3 pro
15	165.5	6.7	140	2 T52468	cytochrome b5 (imp
16	156	6.3	135	2 A86390	hypothetical prote
17	153	6.2	135	2 S49200	cytochrome b5 - co
18	150	6.1	139	2 S46306	cytochrome b5 - co
19	144	5.8	312	2 S77365	hypothetical prote
20	143	5.8	134	2 T14454	cytochrome b5 - w1
21	143	5.8	134	2 T00796	cytochrome b5 - At29
22	139	5.6	137	2 S46307	cytochrome b5 (imp
23	138	5.6	134	2 T52469	cytochrome b5 (imp
24	136	5.5	135	1 CBRP5M	cytochrome b5, out
25	135.5	5.5	120	2 S63052	cytochrome b5 - ye
26	135.5	5.5	121	2 H96631	probable Cytochrom
27	135.5	5.5	318	2 S17197	nitrate reductase
28	134.5	5.5	287	2 T11959	fatty-acid desatur
29	134.5	5.5	877	2 S72541	nitrate reductase

30	133	5.4	424	2 JC5891	omega 6 desaturase
31	132	5.4	124	2 T40071	cytochrome b5 - fl
32	130.5	5.3	438	2 T15039	omega-3 fatty acid
33	128.5	5.2	129	2 T41083	probable cytochrom
34	128.5	5.2	573	1 S06600	L-lactate dehydrog
35	125	5.1	135	2 T09946	cytochrome b5 - so
36	124	5.0	141	2 T15210	probable cytochrom
37	123.5	5.0	909	2 JN0665	nitrate reductase
38	123	5.0	316	2 T19435	hypothetical prote
39	122.5	5.0	904	1 RDNTNT	nitrate reductase
40	122.5	5.0	904	1 RDNTNS	nitrate reductase
41	122.5	5.0	912	1 RDBHNS	nitrate reductase
42	122.5	5.0	915	1 RDBHNS	nitrate reductase
43	122	4.9	352	2 B69901	fatty-acid desatur
44	121	4.9	414	1 S05441	cytochrome b5-rela
45	121	4.9	443	2 T08136	probable omega-6 d

ALIGNMENTS

RESULT 1

T43319
Delta5 fatty acid desaturase (EC 1.14.99.-) T13F2.1 [validated] - Caenorhabditis eleg
C:Species: Caenorhabditis elegans
C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
C:Accession: T43319: T24875
R:Michelson, L.V.; Napier, J.A.; Lewis, M.; Griffiths, G.; Lazarus, C.M.; Stobart, A
FEBS Lett. 439, 215-218, 1998
A>Title: Functional identification of a fatty acid delta5 desaturase gene from Caenor
A:Reference number: 222422; MVID:99059458
A:Accession: T43319
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1447 <MIC>
A:Cross-references: EMBL:AF07896; NID:94003522; PIDN:AAC95143.1; PID:94003523
R:Swimburne, J.
Submitted to the EMBL Data Library, October 1996
A:Reference number: 219947
A:Accession: T24875
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-197, 'VSHIFNN', 198-447 <MIL>
A:Cross-references: EMBL:281122; PIDN:CAB03352.1; GSPDB:GN00022; CESP:T13F2.1
A:Experimental source: clone T13F2
C:Genetics:
A:Gene: CESP:T13F2.1; des-5
A:Map position: 4
A:Intons: 43/3; 80/3; 197/3; 295/3; 318/2; 349/1; 384/3
C:Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 25.5% Score 629, DB 1: Length 447;

Best local similarity 33.0%; Pred. No. 5.2e-45;

Matches 154; Conservative 76; Mismatches 175; Indels 62; Gaps 13;

QY	25	KKDAEAFMLIDMKYDVAREFV-PDHGGSVILTHGKGTQVDFEFH---PRA-AMET 79	118
DB	4	REQHEPEFLIKIDKWCQIDAVLRSHPGSAITTYRNMADTVYFHFHGSKRAYOWLT 63	63
QY	80	LANFVVDIDSDRIDKNDP-----AAEVRK-----LRTLFOSLGYD 118	118
DB	64	ELKKECTQGEPEIPDIDDPKIGDIDVNMGTFINSEKRSQINKSFIDLNRVADESLMD 123	123
QY	119	SSKAYVAFKVSFNICIGLSTVIYAKGQSTLANVLASALLGLFWOCCGLAHDFLHQ 178	178
DB	124	GSPFYTRKI-----LETFILFAFLQYHTY-YLPSALLMGVAMQGLMLLHEFPAHQ 177	177
QY	179	VFODRFWDLEFGAFLGVCVGSFSSMWKDKNHTHAPNHYGEPDIDTPTL-LTWESEHA 237	237
DB	178	LFKNRYINDLASFVGNPLOGFSSGKMEKHNNVHAATNVAGRGDLDLVPYATVAEHL 237	237

QY 238 LEMTSYVPDELTAFMSRRFVLAQMTFFPILTSFALSQCLOSILFLVLPNGAKHPSCAR 297
Db 238 NNYSD-----SWVMFLFMQGHVHTF--MLPFLLSMLOSILFV-----SQ 278
QY 298 VP-----ISLVEQLSLAMHVTYLAATMFLFKIDPNNMLVYFLVSAQVCGNLLATVF 348
Db 279 MPTHTYDYRRTATAYLEBOVGLSLHMANSLGOLY-FLDDWSTRIMFLVSLHLYCGFTLSHV 337
QY 349 SLININMPVLSKEEVAVDMEFTKQIITGRDVPHPFLPAMFTGSLNQLYQIEHLHLPSPMRHN 408
Db 338 TFNHYSEKFAFLSNINMSNVAQLOIMTRMRPGRFTDMLMGSLNQLYQIEHLHLPMPRHN 397
QY 409 FSKIQAPAVETLCKKYNRVYTTGIMCESTAEEVFSRLNEVSKAASKMGK 455
Db 398 LNTWMLPKKEFAANGLPYVAVDDYFTGFMLEIIOFNNINVAKLK 444

RESULT 2

1. linoyleyl-CoA desaturase (EC 1.14.99.25) W08D2.4 - *Caenorhabditis elegans*

N:Alternate names: Delta6 fatty acid desaturase

C:Species: *Caenorhabditis elegans*

C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000

C:Accession: T26280; T37238

R:Swindburne, J.; Almscough, R.
submitted to the EMBL Data Library, March 1996

A:Reference number: 220188

A:Accession: T26280

A:Status: translated from GB/EMBL/DBD

A:Molecule type: DNA

A:Residues: 1-473 <WIL>

A:Cross-references: EMBL:Z70271; PIDN:CA94233.1; GSPDB:GN00022; CESP:W08D2.4

A:Experimental source: clone W08D2

R:Napier, J.A.; Hey, S.J.; Lacey, D.J.; Shewry, P.R.
Biochem. J. 330, 611-614, 1998

A>Title: Identification of a *caenorhabditis elegans* Delta6-fatty-acid-desaturase by heteroduplex analysis

A:Reference number: 221637; MUID:98149727

A:Accession: T37238

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-38, 69-430, 'V', 432-473 <NAP>

A:Cross-references: EMBL:AF031477; NID:g3088519; PIDN:AAC15586.1; PID:g3088520

C:Genetics:

A:Gene: CESP:W08D2.4

A:Map position: 4

A:Introns: 13/3; 39/2; 234/3; 277/3; 378/1; 413/3

A:Superfamily: *Caenorhabditis elegans* Delta6 fatty acid desaturase

A:Keywords: alternative splicing; oxidoreductase; unsaturated fatty acid biosynthesis

	Query Match	21.88;	Score 537;	DB 1;	Length 473;
	Best Local Similarity	30.3%;	Pred. No. 2,9e-37;		
	Matches 145;	Conservative 64;	Mismatches 185;	Indels 82;	Gaps
QY	34	MLIDNK-YYDVRVPPDHGGSV-----ILNHVG-----	K 62		
Db	12	MKVGVGMWLYLSEELVKKHPPGAVIEQYSIPPLKNKIETRGIIITTRGSSNALDILYEYRNS 71			
QY	63	DGTDFVDFDFHPEAM-----ETLANFYVGDIIDSDRPKINDDEFA-AEVK 106			
Db	72	DATIHFAHFGGSSQATKQDLDLKKGHEHDFLEKQLEKRLLDKVDINVASVYDVAOEKK 131			
QY	107	LRTLFQSP-----GYDSSKAYFAKVSFNLCIMGLSTVI-VAKGQSTLANLYSAA 158			
Db	132	MVESEFKRLKRLHDDGLKMKANETFLFKALSTLSIMAFYIQLYGH-----YITSAC 184			
QY	159	LLGLFWQCGGMLANDFLAHQVFQDFRWGDLFGAFLGCVGCGFSSSWMKDKNHTNHANPV 218			
Db	185	LLALAMQOGFGLTHFECHQOQYTKRPLNDPTISLFEFGNFDLGFSDIMWKDKNHNHNAATNV 244			
QY	219	HGEPRDIDTHERLLTWSEHALEMESDVDEELTRMWSKF-----MYLNQTWEPRLISFA 272			
Db	245	IDHGGDIDILAVL-----FPIFG-DLCKYKASFEKALIKIYVQYILYFTAMPIYL 293			

[illegible]

RESULT 3
S68358
Delta8 sphingolipid desaturase (EC 1.14.99.-) [similarity] - common sunflower
C:Species: *Helianthus annuus* (common sunflower)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
C:Accession: S68358
R:Spelling, P.; Schmidt, H.; Heinz, E.
Eur. J. Biochem. 232, 798-805, 1995
A:Title: A cytochrome-b(4)-containing fusion protein similar to plant acyl lipid desaturase
A:Reference number: S68358; MUID:96028121
A:Accession: S68358
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-458 <SPE>
A:Cross-references: EMBL:X87143; NID:g1040728; PIDD:CA60621.1; PID:g1040729
C:Superfamily: cytochrome b5 core homology
C:Keywords: heme; iron; metalloprotein; oxidoreductase
F:16-90/Domain: cytochrome b5 core homology <CB5>
F:51-74/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match	21.7%	Score 534.5	DB 2	Length 458
Best Local Similarity	31.4%	Pred. No. 4.6e-37		
Matches 146	Conservative 71	Mismatches 201	Indels 47	Gaps 14
QY	4	APSVTFTRAEVLNALNECKKDAEAPLMTIDN-----KYVDREFEVNDHRCG	53	
Db	3	SPSI-----EVLNSIA--DGKKYTSKELKKNPNNDLMSILKAYNVTEMAENHPG	54	
QY	54	SVILTHV--GKSDTDEVEDFTHPEAAEETLANFEVGIDESDRIKAKDDFAEYKRTLTQ	112	
Db	55	DAPRLINGQDVTDAFAHPEGTAKHLDKLTG--YHLKQYSDISRDKKLASEPA	111	
QY	113	SLGYDSSKAYAAAFVSFYLCTWG--LSTVIAAKGOSTLANVLASALIGLFMOOCGL	170	
Db	112	KAGMEKK-----GHGVITSLCFVSLLSLACVYGVLYSGSFYTHMLSGAILGAMQIAVL	167	
QY	171	AHDLTHNOVFODRFMGDLFGAFLGVCOCGFSSMMKDKHNTNHAARNVNGEDRPDIDHRL	230	
Db	168	GHDAGHYQMAATRGNNKFRAGIFGNCIGTISIAWMKKTNNHNNHCNSIDYRDLNLRM	227	
QY	231	LWSEHALEMESDVVD-----EELT-RMMSRENVNLQTYRFLISFARLSMLOSILFVL	285	
Db	228	LAVSS--KLFSNITSVFYGRQLTDRPLRAFEVSQYHLYLUMICVARANVLDTQTLILLI	284	
QY	286	PMGQHPKPSGAVPLISLVEOLSLAHNMHTUATLWFLFELIKDRPNMLUYFLVSQAVOCGNLLA	345	
Db	285	-----SKRKIDPRGLINTLTLIFWTFWRLVLSRLPWR--ERAFAVLVSCVYLG-IQH	334	
QY	346	IVFSLNHNGMPYLSKEAVALDMQFETKQITIGRDVPRGLFANMFTGSLVNYOLEHNHLPSPM	405	
Db	335	IQFTLNHNSGDVYVPRPGD--NMFEKQTRGTIDICSSMMQDMQFEGDQFOLEHNHLPRLP	393	
QY	406	RHNEKIQPAVEVLTCKKYNVRYHTTGMEIGTAEVFSRLNEVSKAA	450	
Db	394	RCHLSISIPICRELCKKYNRLPVLSLSPFDANVTTLKTALTAQDA	438	

RESULT 4

T47950
delta-8 sphingolipid desaturase (EC 1.14.99.-) [validated] - Arabidopsis thaliana
N:Alternate names: protein F2A19.180
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C:Accession: T47950.751848
R:De Haan, M.; Maarse, A.C.; Griwell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quer
submitted to the Protein Sequence Database, January 2000
A:Reference number: 224480
A:Accession: T47950
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-449 <DEH>
A:Cross-references: EMBL:AL132962; PIDN:CAE71088.1
R:Spelling, P.; Zaehring, U.; Heinz, E.
J. Biol. Chem. 273, 28590-28596, 1998
A:Title: A sphingolipid desaturase from higher plants. Identification of a new cytochrome
A:Reference number: 222986; MUID:99003197
A:Accession: T51848
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-449 <SPE>
A:Cross-references: EMBL:AJ224161; PIDN:CAA11858.1
A:Experimental source: cultivar Columbia; mainly green parts, some flowers, few roots
C:Genetics:
A:Gene: slt1
A:Map position: 3
A:Note: F2A19.180
C:Function:
A:Description: (EC 1.14.99.-); delta-8 sphingolipid desaturase [validated; MUID:99003197
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 21.2%; Score 522; DB 2; Length 449;
Best local similarity 30.2%; Pred. No. 5e-36;
Matches 137; Conservative 82; Mismatches 190; Indels 44; Gaps 15;

11 TRAEVLAELNKGKDAEAFILMIIDNKYVDREPRDPRGG-SVLTTHVGKDGTVDPD 69
DB 5 TEKRYITNEGLKHNKSGD--LWIAIOGKAYNVDWIKTHPRGGDTVLNLVGGDVIDAFT 62
QY 70 TFRPEAMETLANFYVDIDESDRDIKNDPFAAEVRKRLTFLQSLGYDSSKAYAFKVS 129
DB 63 AFRPRGAMHHLDLFTG---YHTRDQVSEVSDYRMAEFKRLGLFEKKGHTVLTTLA 119
QY 130 ENICINGLSTVIYAKKQISTLANVLSALLGLFMQCGMLAHDFLHHQVQDRFWGDLF 189
DB 120 FVAAME--LGLVGLVLACTSVFAHQIAALLGLMIQSAVIGHDSGHYVINSKSY-NRE 176
QY 190 GARLGVG-CGGFSSSMKKDKNHTNHARPVNHGDDPDIDTFLTLWSHNALEMSDVP--- 245
DB 177 AQLISGCLTGISIAWKKWTHNAHNLACNSLDYDPDIDHPRVAVS--TKFFSSLTSRF 233
QY 246 -DEELT-RMMSRPMVLNQTWFFPIISFARLSMCIOSILFLFPGAGAHKPSGARVPTSLV 303
DB 234 YDKRLTFDPARLRVLSQHTFYRVKMGFRKINLEIQTFLLF-----SKREVPRAL 265
QY 304 EQLSLAMHWTYATMFLFKIDRVNMLVYLVSOACGNLAIVFSINH-----NGMPV 357
DB 286 NFAGILVFTWTFPLVLSCLPNNBERF--FFVETSFVTALQHOFTLNRAADVVYVPT 343
QY 358 ISKEEAVNDMEFFKOITIGDVRHGLFANMFTGSLNVOIEHHLPSPMRNFSKIQAV 417
DB 344 GS-----DMFEKQAAGTIDISCRSTMDWFFGGLDFOLHNLHLPRLRCHLRKVSVVO 396
QY 418 TLCKKYVNRHTTGMIEGTAEVSRLENSKAA 450
DB 397 ELCKKHNLPYRSMSWE--ANVLT-INTLKTAA 426

RESULT 5
T50555

delta-8 sphingolipid desaturase [imported] - rape
C:Species: Brassica napus (rape)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 15-Sep-2000
C:Accession: T50555
R:Spelling, P.; Zaehring, U.; Heinz, E.
J. Biol. Chem. 273, 28590-28596, 1998
A:Title: A sphingolipid desaturase from higher plants. Identification of a new cytochrome
A:Reference number: 222986; MUID:99003197
A:Accession: T50555
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-449 <SPE>
A:Cross-references: EMBL:AJ224160; PIDN:CAA11857.1
A:Experimental source: cultivar Drakkar
C:Genetics:
A:Gene: slt1

Query Match 20.4%; Score 502; DB 2; Length 449;
Best local similarity 31.0%; Pred. No. 2.4e-34;
Matches 130; Conservative 72; Mismatches 193; Indels 24; Gaps 12;

36 IDNKYVDREPRDPRGG-SVLTTHVGKDGTVDPFTRPEAMETLANFYVDIDESDRD 94
DB 28 IQCKYVDVSHWVSKHSGGEAAILNLGQDVTDAFIAVHPGTARHLENLHNG--YHVKD 84
QY 95 IKNDPFAAEVRKRLTFLQSLGYDSSKAYAFKVSFLCIMG-LSTVIYAKKQISTLAN 153
DB 85 HHVSDVSRDPRRLAERSKRGDLFGKHVTLTYLT--CYAAMLAAYGVVACTSTMAH 141
QY 154 VLSAALIGLFMOCCGMLAHDFLHHQVQDRFWGDLFGARLGVGCGFSSSMKKDKNTHH 213
DB 142 LISAVILGLMLIQSAVYGHDSGHYNTSTPKCKLVQLVLSGNCITGISIMWKTHNAH 201
QY 214 AARPVHGEDPDIDTFLTLWSHNALE-MESDVPDEELT-RMMSRPMVLNQTWFFPIISF 271
DB 202 ISCNSLDHDLDLHPIQVLAIVSNKFFKSMSTSPYGRKLTFLPRFLTSYOHWSFPTMCV 261
QY 272 ARLSMCIOSILFPLNPGAKRPGARVPSLVBQLSLAMHNTWLANMFLFIDPVMVLV 331
DB 262 GRINLFTQTLLEF-----SRRYVDRALNAGILVWTMF-PLVSEFLPMMQERTI 312
QY 332 YFLVSOAVCGNLIAIVFSLNHNCPVLSKEEAVNDMEFFTKOITIGRDVHGLFANMFTGG 391
DB 313 FVLISMAVTA-IQHVQCLNHFADVYTPRPNGC-DMFEKQTAGTIDISCRSTMDWFFGG 370
QY 392 LNVQIEHNLFPSPMRNFSKIQPAVETLCKKYVNRHTTGMIEGTAEVSRLENSKAA 450
DB 371 LQVLEHNLHLPRLRCHLRVSPVDELCKKHNLPYRSLSMWE--ANVLT-LPTLRKAA 426

RESULT 6
A84900
hypothetical protein At2g46210 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: A84900
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.T.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
eaus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Saltsberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083467
A:Accession: A84900
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-449 <STO>
A:Cross-references: GB:AE002093; NID:g3702328; PIDN:AAC62885.1; GSPDB:GN00139
C:Genetics:
A:Map position: 2

[illegible]


```
Db 188 YKSKSNHVIHKEFVIGHLKASASAMNHRHFOHAKENIFHKPDIKSLHVFLGEMOPL 247
OY 236 -----HALEMFSQVDEDELTMMKSRF-----VNLQOTW--FFPILISFARLS 275
Db 248 EYKSKKIKLUPYHNOHYEFLIGRPPLIPMFYOQITMTIRRDWDLMAALSYARFP 307
OY 276 WCLQSLIFLVPNGQANRPSGARVPISLVEQLSLAMHTWYLATMFLIKDPVNLVYFLV 335
Db 308 YTIIPFYGIL-----GALVFLNIR--FLESHMFVWYQW----- 340
OY 336 SQAVCGNLAIIVESLNHNGRPVYSKEAVDMDEFTKOITGRDVPGLFAMWFTGLINYQ 395
Db 341 -----NHIMEIDLDHY-----RDMFSQLATCNEVQGFNDMFGSHLNFQ 382
OY 396 IEHHLFSPMRHNSKIQPAVEFLCKKYNRYHTTGMEICTAEVFSUNE 445
Db 383 IEHHLFPTMRHNLKTLAPLVKSLCAKHGIEYOEKRPILLRLDLIVSSLKK 432

RESULT 9
JC7556
linoleoyl-CoA desaturase (EC 1.14.99.25) - Mucor rouxi
N/Alternate names: delta6-desaturase
C/Species: Mucor rouxi
C/Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 31-Mar-2001
C/Accession: JC7556
R/Laoteng, K.; Manontarat, R.; Tanticharoen, M.; Cheevadhanarak, S.
Biochem. Biophys. Res. Commun. 279, 17-22, 2000
A>Title: Delta6-desaturase of Mucor rouxi with high similarity to plant delta6-desaturase
A:Reference number: JC7556; MOID: 20563795
A:Accession: JC7556
A:Molecule type: DNA
A:Residues: 1-523 <LMO>
A:Cross-references: GB:AF290983
A:Experimental source: strain ATCC 24905
C/Comment: This enzyme, a membrane-bound key enzyme, is responsible for the transformation of
C:keywords: transformation; oxidoreductase

Query Match 17.5%; Score 432; DB 3; Length 523;
Best Local Similarity 25.2%; Pred. No. 2.2e-28;
Matches 134; Conservative 85; Mismatches 196; Indels 116; Gaps 20;

OY 9 TFFR-AEVLAAELNECKKDAEAPELMIDNKYVDREFPDGGSGVIL--THGSKGTD 66
Db 14 TSTRSSNIVIEKFOELIKOGDSYF--TYROKYVRVNNFMKHPGSAALSGRDVTD 71
OY 67 VFDTFHPAAMETLANFY-VGD----- 87
Db 72 EIRFMHPRQYUEKILNLYCGDVMRDVIRASMKQHTFTKPKEDKVLVATWEGFTVQ 131
OY 88 -IDES-----DRDIKNDFAEVRKRLTFLFQSLGYDSSKAYAFKV 128
Db 132 AYDDAIDQLDKHNSHDLIKDAVLQKDLNGDQIRNAUKRLAEIYAKGLF--KCNV-WKY 187
OY 129 SFNLCIMGLSTVIYAKV--GQSTLANVLSAALLGLFMQCCGLADLHNOVQ---- 181
Db 188 ARECCRYTL-LIFLSLMTFLKGTETWYMGAAAFMAFMQOLVETADAGINNETGKSEI 246
OY 182 DRFMGDLFGAFLGVCQGFSSMMKDKHNTNHAAPVNGEPRDITPRLTLTWSHALEM 241
Db 247 DNYIGVIANFIGLSLG-----MKKDNHNVNHTYTNPREHDPDQIHYEFMAIT--TKRF 299
OY 242 SDVPDEELTRMM-----SRPMVNLQTFYRPLISFARLSMCLQSLFVLPNGQANRPSGA 296
Db 300 NNITSTYKKRVLPRDASREFVRHQHLYLLISFGRFNLHRSFAVLL-----TCK 351
OY 297 RVPISLVEQLSLAMHTWY--LATMFLTKDPV--NMLVFLVLSQAVCGNLAIIVESLNH 352
Db 352 NVRTRLTELGLITFFEFWFGSLSTL-----PTMNIIRIAYIVSYMLTGPRLHQLTISH 405
OY 353 NGMPVISKEAVDMDEFTKOITGRDVPGLFAMWFTGLINYQIEHHLFSPMRHNSKI 412
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Db 406 FGMS--TEDGPRDEPPFAKMLRTTMDVDCSEMHQWFGHGLQYQVHHLFRLPRHNRQC 463
OY 413 QPAVETLCKKYNRYH-----TTGMEICTAEVFSRLNEVSKAASK 453
Db 464 VPLVKKFCDEGLHYMYNFSGTNGVVLFTLKSVDQVGFANVEYAKSNAEI 514

RESULT 10
T36617
probable Delta6 fatty acid desaturase (EC 1.14.99.-) SCH35.42c [similarity] - Strepto
C/Species: Streptomyces coelicolor
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
C/Accession: T36617
R/Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Randleam, M.A
submitted to the EMBL data library, June 1999
A:Reference number: Z21610
A:Accession: T36617
A:Status: preliminary; translated from GB/EMBL/DDBV
A:Molecule type: DNA
A:Residues: 1-345 <OLIT>
A:Cross-references: EMBL:AL076610; PIDN:CA844385.1; GSPDB:GN00070; SCQEDB:SCH35.42c
A:Experimental source: strain A3(2)
A:Gene: SCQEDB:SCH35.42c
C:keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 17.1%; Score 422.5; DB 2; Length 345;
Best Local Similarity 32.3%; Pred. No. 8.1e-28;
Matches 113; Conservative 50; Mismatches 138; Indels 49; Gaps 14;

OY 94 DIKNDFAEVRKRLTFLFQSLGYDSSKAYAFVFS---FNLCIMGLSTVIYAKMGOTS 149
Db 11 DTPEGDFARLSKV-----ADAGLLGRRGYITTLITAVTGILYAGMAFVLVGSMM--- 63
OY 150 TLAVNLASAALLGLFMQCCGLADLHNOVQDRFMGDLFGAFLGVCQGFSSMMKDKH 209
Db 64 TLA---IAAFLAVMGVALVAHDMARQVRRRASSELGR-IGASIGMSYGMQDKH 119
OY 210 NTHNAPNVHGEDPDITPRLTLTWSHALEMFSVPDEE-----LTKMSKFFVNLQTF 264
Db 120 TRHNANPTEDLDIPG-DLLVMS-----PDQARAATGLPRLGRW---QAF 164
OY 265 YEPILISFARLSMCLQSLFVLPNGQANRPSGARVPISLVEQLSLAMHTWYLATMFL 324
Db 165 FEPILT-----LEGFNLHASGRA--MANRRRLRRALDGLLACAVLTALFVVL- 214
OY 325 DPVNLVYFL-VSQAVCGNLAIIVESLNHNGMPVYSKEAVDMDEFTKOITGRDVPGL 383
Db 215 -PRGMATAFLAVHQCFLGVYLGSAFARNHKMPLTADDR--PDLRQVLTSSNVNGCL 271
OY 384 FANWFTGLNYQIEHHLFSPMRHNSKIQPAVEFLCKKYNRYHTTGMT 433
Db 272 FTDLALGLNQHIEHLPSPMSPNLKRAIYVRRCDLGVDAEYGLV 321

RESULT 11
S54809
linoleoyl-CoA desaturase (EC 1.14.99.25) - Spirulina platensis
N/Alternate names: Delta6-desaturase
C/Species: Spirulina platensis
C/Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jun-2000
C/Accession: S54809
R/Tasaka, Y.
submitted to the EMBL data library, May 1995
A:Accession: S54809
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-368 <TAS>
A:Cross-references: EMBL:X87094; NID:9809109; PIDN:CA60573.1; PID:9809110
C:keywords: oxidoreductase; unsaturated fatty acid biosynthesis
```

Query Match 9.2%; Score 227; DB 2; Length 368;
 Best Local Similarity 25.9%; Pred. No. 2.2e-11;
 Matches 89; Conservative 49; Mismatches 142; Indels 64; Gaps 17;

137 LSTVIYAKV-----GQSTLANVLAALGLFMOQCGW-LAHDFLHNOFQDRFM 185
 43 LKTAIIILAVVSAWTFVVGPRVLMKLLGCTVIGFVSAVGENISHDG-NHGGYKTYOM 101
 186 GDLFGAFLGVCVCG--GFSSSWKKDKHNT-HNAAPVHGEDPDIDTHPLTWSEHALEM 241
 102 VN-----YLSGLTIDAIGVSYLMKFRHNVLIHHTYTNILGHDEVI-----HCDLV 147
 242 SDVDEELRMSRFVNLQMTWFFPILSFARLSMCLQSLFVLPNGOAKH---PEGARV 298
 148 RNSPSEMY-RWYHRY---OHMTFVFPPIPYWMSIAVQTMLEFRQYHDEIPSPVW 202
 299 PISLVEQLSLAMHMTWYLATMFLFIK-----DPVNMVLYFLVSOAVCGNLAIVFSLNHN 353
 203 DIATL-----LAFKAFVAVFLILIPAVGYSPLFVAVIGASIVYMTNGLVACVFMALH- 255
 354 GMPVYSKEAVDMD-----FTTKOITIGRDVHP-GLFANMFTGGLNYQIEHHLPSPMP 405
 256 ---VIEPAEFLPDNLHIDEMALIAQVKTVDFAFPNNPIINWVGGLNYQVTHHLPFHC 312
 406 RHNEFSKIOPAVETLCKKNVRY--HTTGMIEGTAEVFSRLNEVS 447
 313 HIHPKIAPIIAVECEBFVNTAVHOT-FFGALANYSMLWKMS 355
 DB

RESULT 12

S3157
 Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - *Synechocystis* sp.
 C:Species: *Synechocystis* sp.
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
 C:Accession: S3157; S76243
 R:Reddy, A.S.; Nuccio, M.L.; Gross, L.M.; Thomas, T.L.
 Plant Mol. Biol. 22, 293-300, 1993
 A:Title: Isolation of a Delta(6)-desaturase gene from the cyanobacterium *Synechocystis* sp.
 A:Reference number: S3157; MUID:93283633
 A:Accession: S3157
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-359 <RED>
 A:Cross-references: GB:LI1421; NID:9349562; PIDN:AA27286.1; PID:9349563
 R:kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; MiyaJima, N.; O. K.; Okumura, S.; Shimp, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.
 A:Reference number: S74322; MUID:97061201
 A:Accession: S76243
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-359 <KAN>
 A:Cross-references: EMBL:D90914; GB:AB001339; NID:g1653477; PIDN:BA18502.1; PID:d101923
 A:Experimental source: PCC 6803
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 8.5%; Score 210.5; DB 2; Length 359;
 Best Local Similarity 25.7%; Pred. No. 5.2e-10;
 Matches 83; Conservative 55; Mismatches 124; Indels 61; Gaps 16;
 137 LSTVIYAKVQSTLANVLSA-----ALIGLFWQCGMILA-----HDFLHNOV 179
 42 LKTLIIIVLW-LFSAMAFVLEAPYIFVRLG-----CWLALALALAFSNVGDANHNAY 95
 180 FQDRFMDLFGAFLGVCVCGFSSSWKKDKHN-THAAPVHGEDPDIDTHPLTWSEHAL 238
 96 SSNPHTIRVILGMYDFV--GLSSFWRVRRHNYLIHHTYTNILGHDEVIH-----GDGAV 146
 DB

239 EMEFSDVDEELRMSRFVNLQMTWFFPILSFARLSMCLQSLFVLPNGOAKHPS-GAR 297
 147 RM---SPEOHVGYI-RF---QOFTWGLYLFIPYWFVLYVYLWNGKGIHDKIRPF 198
 298 VISLVEQLSLAMHMTWYLATMFLFIKDPV-NMIVYFLVSOAVCGNLAIVFSLNHNHNGMP 356
 199 OPLELASLIGILMLMGVYFGILPAGFISIPREVLIGASTYMTYIGVCTIMLAH----- 254
 357 VISKEE-----AVDMFTTKOITIGRDV--HPLFANMFTGGLNYQIEHHLPSPM 404
 255 VLESTFELTPDESGAIDEMALICQIRTNANFATNPP-FMMVFCGGLNHQVTHHLPFNI 312
 405 PRHNEFSKIOPAVETLCKKNVRY 427
 313 CHIHPIOLENIIKDVCOERGVET 335
 DB

RESULT 13

B83034
 conserved hypothetical protein PA4888 [imported] - *Pseudomonas aeruginosa* (strain PAO
 C:Species: *Pseudomonas aeruginosa*
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: B83034
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Adam, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapid, K.; L
 :; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an opportunistic pa
 A:Reference number: A82950; MUID:20437337
 A:Accession: B83034
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-370 <STO>
 A:Cross-references: GB:AE004902; GB:AE004091; NID:9951162; PIDN:AA08273.1; GSPDB:GN
 A:Experimental source: strain PAO1
 C:Genetics:
 A:Gene: PA4888

Query Match 7.0%; Score 173.5; DB 2; Length 370;
 Best Local Similarity 21.0%; Pred. No. 6.9e-07;
 Matches 80; Conservative 64; Mismatches 142; Indels 95; Gaps 18;

92 DEDIKNDPFAA-----EVKRLTFLQSLGYSKAYFAFKVSPNLCJWGSLTVIAKMG 146
 12 DRELTPEDQLAAGAEIDALRLKTL-ADLG-ADDARTIRRVRAVYCCSGRALLMFGHL 69
 147 QSTLANVLSAALGLFMOQCG-----WLAHDFLHNO---VFODRFMDLFGAFLGVC 197
 70 PPTWL-----LGSILLGL-----GKILENMELGHNHVGQYDMNDEFFAGRAVEMDIAG-- 119
 198 QGFSSSWKKDKHN-THAAPVHGEDPDIDTHPLTWSEHALEMSDVDEELRMSRF 256
 120 ---PSDFMRHTNHHTYTNVIGKDDV-----GYGVRLPE-----ORWRF 161
 257 NVLNGWFEPFLSFARLSMCLQSLF-----VLPNGOAKHPSGAR-----VISLVEQL 306
 162 YKQPKLV-----TLQALLFOYAVAIQHRLDKYAKGRIDKRAELMPLRLRLRA 209
 307 SLAMHMTWYLATMFLFIK-----PVNMLVYFLVSOAVCGNLA-----IVFSLNH 352
 210 KIGRQWT-----KYLLEPFLGLGFAAGFAGVFNGLNLANVRLMTFTVIFCGHF 259
 353 NGMPVYSKEAVDMD-----FTTKOITIGRDVHPGLFANMFTGGLNYQIEHHLPSPMPRHN 408
 260 TEKAVVFPFVSEGETRGHWYLRQLRGSSNLGGLFHLITGNLSHOIEHHLPDLPARR 319
 409 FSKIOPAVETLCKKNVRYHT 429
 320 YVALSREVRERIRRYGQTYNS 340
 DB

RESULT 14
G70590
probable desA3 protein - Mycobacterium tuberculosis (strain H37Rv)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: G70590
R:Coile, S.T.; Brosch, R.; Parthill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A:Authors: Soares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MID:9825987
A:Accession: G70590
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-427 <COL>
A:Cross-references: GB:295121; GB:AL123456; NID:g3261742; PIDN:CAB08330.1; PID:e314467;
A:Experimental source: strain H37Rv
C:Genetics:
A:Gene: desA3

Query Match 6.9%; Score 169.5; DB 2; Length 427;
Best Local Similarity 23.5%; Pred. No. 1.8e-06;
Matches 91; Conservative 68; Mismatches 138; Indels 91; Gaps 24;

OY 85 VGDIIDE-----SDRDKNDDFAAEVRYKL-FTLFQSLGYDSS-----KAYYAFKVSFNLG 133
DB 3 ITVDYVFANHLTDADIEH--LAELDAIRROVEESRGERRDARYIRRTTAORALEVSGRL 60
OY 134 IWGLSTVIYAKWGOTSTL--ANVLSAALLG--LFWOOCGLANDFLHNOYFODRFMGDLF 189
DB 61 LAG-SSRRRLAMWAGLGLGAKIENNEIGHNVHGMNDPEIHSTWE--W-DMS 115
OY 190 GATLGGVCGGSSSMWKDKIN-THNAARNVNGEDPDIDTNRPLTWSEHLEMFSDVDEE 248
DB 116 G-----SSKHWRYTHNFVHNKRYTNILGMDDVGYGL-----R 148
OY 249 LTR--MMSRFMVNLOTGFYRPIISFARLSW--CLOSI-LFVLRPGOAHK----- 292
DB 149 VTRDQRRKRNTIFNVNNTLALIGF---EWGVALOHLEIGKIFKGRADREAKTRLREPS 205
OY 293 -PSGARV---PISLVEOLSLAMHTWYLAFTFKDPVNLVYFLVSOAV--CGNLAI 346
DB 206 AKAGROYFKDYVAFPALTSFGAT-YRSTL--TANVVANVINWMSNAVIFCGHF--- 258
OY 347 VFSLNHGMFVSKREAVDM--DEFTKOITGSDVHFGLEFANWFGLNYQIEHNLPS 403
DB 259 -----PDGAKEFTKTDIGEPKQGYLRQMLGSANFNAGPALRFMSGMLCHQIEHNLYPD 313
OY 404 MPRHNFESKIOPAVETLCKKYNVRHTTG 431
DB 314 LPSNRLHEISVRVREVCDDYLPY-TTG 340

RESULT 15
T52468
cytochrome b5 (imported) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 01-Dec-2000
C:Accession: T52468
R:Fukuchi-Mizutani, M.; Mizutani, M.; Tanaka, Y.; Kusumi, T.; Ohta, D.
A>Title: Microsomal Electron Transfer in Higher Plants: Cloning and Heterologous Expression
A:Reference number: Z25274
A:Accession: T52468
A:Status: preliminary;
A:Molecule type: mRNA
A:Residues: 1-140 <FNK>
A:Cross-references: EMBL:AB007802; PIDN:CAB17232.1
C:Superfamily: cytochrome b5; cytochrome b5 core homology
C:Keywords: heme; iron; metalloprotein

F:40,64/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 6.7%; Score 165.5; DB 2; Length 140;
Best Local Similarity 34.3%; Pred. No. 9.8e-07;
Matches 48; Conservative 16; Mismatches 43; Indels 33; Gaps 6;
OY 8 RTFTRAEVLNAEALNEGKDAEAPFLIIDNKVYDVREVPDHPG--SVILTHVKGQDGD 66
DB 6 KVFLLSEV---SQHSSAKDC---WIVIDGKYVDVTKFLDDHFGDGVILSTGKDADT 57
OY 67 VFTFPEAAMETLANFYVDIDESDRDI-----KNDPFAAEVRYKL 108
DB 58 DFEEDVGHSSSTAKAMLDEEYVGDDITATVPYAKFVPTSTRAVATQDKSSDFVILQLQFL 117
OY 109 TLFQSLG-----YYDSKA 122
DB 118 VPLILGLAGIRIRYTTKTKA 137

Search completed: August 9, 2001, 20:26:03
Job time: 242 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 9, 2001, 20:36:48 ; Search time 28.86 Seconds

(without alignments)
5.935 Million cell updates/sec

Title: US-09-367-013b-2-COPY_39_43
Perfect score: 26
Sequence: 1 KVDV 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	89	Y916_METUA	Q58326 methanococ
2	26	100.0	120	CYB5_YEAST	P40312 saccharomyc
3	26	100.0	132	CYB5_BOROF	O04354 borago Offi
4	26	100.0	134	CY51_ARATH	O42342 arabidopsis
5	26	100.0	134	CYB5_BRAOL	P40934 brassica ol
6	26	100.0	135	CYB5_CUSRE	P49097 cusculta ref
7	26	100.0	136	CYB5_TORAC	P49096 nicotiana t
8	26	100.0	274	YD41_SCHPO	Q10343 schizosacch
9	26	100.0	323	TRXB_AQUAE	O66790 aquilex aeo
10	26	100.0	395	FLAD_RHIME	O52942 rhizobium m
11	26	100.0	410	PSY_MAIZE	P49086 zea mays (m
12	26	100.0	423	PSY_NARPS	P33787 narcissus p
13	26	100.0	550	THDH_ARKAD	O42615 arxula aden
14	26	100.0	553	DPOL_BPPRD	P10479 bacterioph
15	26	100.0	601	PEF1_LACIA	P41424 lactococcus
16	26	100.0	602	PEF2_LACIA	P44876 lactococcus
17	26	100.0	645	YOB1_CAEEL	P34617 caenorhabdi
18	26	100.0	679	NAD6_MYCTU	P11911 mycobacteri
19	26	100.0	828	CAN_DROME	Q11002 dtrosophila
20	26	96.2	44	RIP3_MOMCH	P24817 momordica c
21	26	96.2	98	PSAD_SYNP6	P33076 synechococc
22	26	96.2	156	AP19_YEAST	P35181 saccharomyc
23	26	96.2	174	CALB_NEUCR	P87072 neurospora
24	26	96.2	177	CALB_NAAGR	P42322 naegleria g
25	26	96.2	201	YMW3_YEAST	Q04772 saccharomyc
26	26	96.2	207	MODA_BPT4	P39423 bacterioph
27	26	96.2	210	RAB8_DDISM	P22128 discopyge o
28	26	96.2	286	RIP2_MOMBA	P29339 momordica b
29	26	96.2	287	MCES_SPKVA	O08512 swinepox vi
30	26	96.2	306	FLIH_BORBU	P52611 borrelia bu
31	26	96.2	315	TRXB_BACSU	P08080 bacillus su
32	26	96.2	319	TRXB_LISMO	O32823 listeria mo
33	26	96.2	338	YYAD_BACSU	P37520 bacillus su

ALIGNMENTS

34	25	96.2	366	1	DHLE_THEIN	O6030 thermoactin
35	25	96.2	384	1	SCS7_YEAST	Q03529 saccharomyc
36	25	96.2	386	1	ICSA_XENIA	P55865 xenopus lae
37	25	96.2	418	1	GSA_ARCFU	O29027 archaeoglob
38	25	96.2	420	1	GATZ_ECOLI	P37191 escherichia
39	25	96.2	427	1	AROA_STRPN	Q35400 streptococc
40	25	96.2	484	1	AMYA_ASPNG	P56271 aspergillus
41	25	96.2	546	1	SVR_THEMA	Q9X0H8 thermotoga
42	25	96.2	717	1	VGLH_HSVSA	P16492 herpesviru
43	25	96.2	917	1	SVL_CAMEJ	P41257 campylobact
44	25	96.2	931	1	DAP1_YEAST	P33894 saccharomyc
45	25	96.2	1248	1	TOPG_STULAC	Q08582 sulfolobus

RESULT 1						
ID	Y916_METUA	STANDARD:	PRT:	89 AA.		
AC	O58326:					
DT	15-JUL-1998 (Rel. 36, Created)					
DT	15-DEC-1998 (Rel. 37, Last sequence update)					
DT	15-DEC-1998 (Rel. 37, Last annotation update)					
DE	HYPOTHETICAL PROTEIN M0916.					
GN	M0916.					
OS	Methanococcus jannaschii.					
OC	Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;					
OC	Methanococcus.					
OX	NCBI_TaxID=2190;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN-JAL-1 / DSM 2661 / ATCC 43067;					
EX	MEDLINE=96337999; PubMed=688087;					
RA	Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,					
RA	Sulton G.G., Blake O., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,					
RA	Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,					
RA	Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,					
RA	Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,					
RA	Uutterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,					
RA	Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,					
RA	Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;					
RT	"Complete genome sequence of the methanogenic archaeon, Methanococcus					
Jannaschii."						
RL	Science 273:1058-1073(1996).					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration					
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/					
CC	or send an email to license@isb-sib.ch).					
CC						
DR	EMBL: U67535; AAB98921.1; -					
DR	TIGR: M0916; -					
KW	Hypothetical protein.					
SO	SEQUENCE 89 AA; 9673 MW; ADA40C45D1D858F9 CRC64;					
Query Match	100.0%;	Score 26;	DB 1;	Length 89;		
Best Local Similarity	100.0%;	Pred. No. 21;				
Matches	5;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
OY	1 KVDV 5					
Db	23 KVDV 27					
RESULT 2						
ID	CYB5_YEAST	STANDARD:	PRT:	120 AA.		
AC	P40312;					

DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CYTOCHROME B5.
 GN CYB5 OR YNL111C OR N1949.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 NX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FL100;
 RX MEDLINE=94237477; PubMed=8181746;
 RA Truan G., Epinat J.-C., Rougeulle C., Cullin C., Pompon D.;
 RT "Cloning and characterization of a yeast cytochrome b5-encoding gene
 which suppresses ketoconazole hypersensitivity in a NADPH-P-450
 reductase-deficient strain.";
 RL Gene 142:123-127(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97245296; PubMed=9090055;
 RA de Antoni A., D'Angelo M., Dal Pero F., Sartorello F., Pandolfo D.,
 RA Pallavicini A., Lanfranchi G., Valle G.;
 RT "The DNA sequence of cosmid 14-13b from chromosome XIV of
 Saccharomyces cerevisiae reveals an unusually high number of
 overlapping open reading frames.";
 RL Yeast 13:261-266(1997).
 CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
 CC INVOLVED IN SEVERAL STEPS OF THE STEROL BIOSYNTHESIS PATHWAY,
 CC PARTICULARLY IN THE 4-DEMETHYLATION OF THE 4,4'-DIMETHYL
 CC ZYMOSTEROL.
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 CC -----
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 CC -----
 CC EMBL: L22494; AAA67468.1; -;
 CC EMBL: Z69382; CAA93396.1; -;
 CC EMBL: Z71387; CAA93990.1; -;
 CC PIR: S47919; S47919.
 CC HSSP: P04166; 1B5M.
 CC SGD: S0005055; CYB5.
 CC InterPro: IPR001199; -;
 CC Pfam: PF00173; heme_1; 1.
 CC PRINTS: PR00363; CYTOCHROME_B5.
 CC PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 CC PROSITE: PS02555; CYTOCHROME_B5_2; 1.
 CC Electron transport; Transmembrane; Heme; Microsome.
 CC BINDING 37 37 HEME LIGAND (BY SIMILARITY).
 CC BINDING 61 61 HEME LIGAND (BY SIMILARITY).
 CC BINDING 98 118 POTENTIAL.
 CC TRANSMEM 17 17 E -> Q (IN REF. 1).
 CC CONFLICT 17 17
 CC SEQUENCE 120 AA; 13297 MW; 598BEF2A6730CAD19 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 120;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKYDV 5
 | | | | |
 DB 26 KKYDV 30

RESULT 3
 ID CYB5_BOROF STANDARD; PRT; 132 AA.
 AC 004354;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CYTOCHROME B5.
 OS Borago officinalis (Borragae) (Borragae).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
 OC euasterids I incertae sedis; Boraginaceae; Borago.
 NX NCBI_TaxID=13363;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97268723; PubMed=9108131;
 RA Sayanova O., Smith M.A., Lapinskas P.A., Stobart K., Dobson G.,
 RA Christie W.W., Shewry P.R., Napier J.A.;
 RT "Expression of a borage desaturase cDNA containing an N-terminal
 cytochrome b5 domain results in the accumulation of high levels of
 delta6-desaturated fatty acids in transgenic tobacco.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
 CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
 CC INVOLVED IN SEVERAL STEPS OF THE STEROL BIOSYNTHESIS PATHWAY,
 CC PARTICULARLY IN THE 4-DEMETHYLATION OF THE 4,4'-DIMETHYL
 CC ZYMOSTEROL.
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 CC -----
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 CC -----
 CC EMBL: U79011; AAC49701.1; -;
 CC HSSP: P00171; 1CYO.
 CC Mendel: 15843; Borof; 1218; 15843.
 CC InterPro: IPR001199; -;
 CC Pfam: PF00173; heme_1; 1.
 CC PRINTS: PR00363; CYTOCHROME_B5.
 CC PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 CC PROSITE: PS02555; CYTOCHROME_B5_2; 1.
 CC Electron transport; Transmembrane; Heme; Microsome.
 CC BINDING 37 37 HEME LIGAND (BY SIMILARITY).
 CC BINDING 61 61 HEME LIGAND (BY SIMILARITY).
 CC TRANSMEM 104 124 POTENTIAL.
 CC SEQUENCE 132 AA; 14556 MW; 96EF72A06F2E8C5B CRC64;

Query Match 100.0%; Score 26; DB 1; Length 132;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKYDV 5
 | | | | |
 DB 26 KKYDV 30

RESULT 4
 ID CY51_ARATH STANDARD; PRT; 134 AA.
 AC 042342; Q9SB05;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CYTOCHROME B5 ISOFORM 1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.

```

OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX PubMed=9880378;
RA Fukuchi-Mizutani M., Mizutani M., Tanaka Y., Kusumi T., Ohta D.;
RT "Microsomal electron transfer in higher plants: cloning and
RT heterologous expression of NADH-cytochrome b5 reductase from
RT Arabidopsis."
RL Plant Physiol. 119:353-361(1999).
RN [2]
RP SEQUENCE OF 1-113 FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Cooke R., Laudie M., Raynal M., Delseny M.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
CC OXYGENASES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC -----
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CC -----
DR EMBL; AB007801; CAB17231.1; -.
DR EMBL; F20001; CAA23377.1; -.
DR Mendel; 6696; Arath.1218:6696.
DR HSSP: P00171; 1CYO.
DR InterPro: IPR001199; -.
DR Pfam; PF00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROME_B5_1; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
DR Electon transport; Transmembrane; Heme; Microsome; Multigene family.
FT BINDING 40 40 HEME LIGAND (BY SIMILARITY).
FT BINDING 64 64 HEME LIGAND (BY SIMILARITY).
FT TRANSMEM 107 127 POTENTIAL.
FT CONFLICT 1 3 MSS -> ARA (IN REF. 2).
SQ SEQUENCE 134 AA; 15084 MW; 9CC01C60F7C873FD CRC64;

Query Match 100.0%; Score 26; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDYD 5
DB 29 KVDYD 33

RESULT 5
CYB5_BRAOL STANDARD; PRT; 134 AA.
AC P40934;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CYTOCHROME B5.
GN CYB5.
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
RN [1]
RP SEQUENCE FROM N.A.; AND SEQUENCE OF 6-47 AND 75-89.
RC STRAIN=CV. CAULIFLORA;

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RA Kearns E.V., Keck P., Somerville C.R.;
RT "Nucleotide sequence of cDNA for cytochrome b5 from cauliflower
RT (Brassica oleracea L.)";
RL Plant Physiol. 99:1254-1257(1992).
CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
CC OXYGENASES.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC -----
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CC -----
DR EMBL; M87514; AAA32990.1; -.
DR HSSP: P00171; 3B5C.
DR InterPro: IPR001199; -.
DR Pfam; PF00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROME_B5_1; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
DR Electon transport; Transmembrane; Heme; Microsome.
FT BINDING 40 40 HEME LIGAND (BY SIMILARITY).
FT BINDING 64 64 HEME LIGAND (BY SIMILARITY).
FT TRANSMEM 107 127 POTENTIAL.
FT VARIANT 5 5 K -> N.
SQ SEQUENCE 134 AA; 15062 MW; 764DC24A4CDD591 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDYD 5
DB 29 KVDYD 33

RESULT 6
CYB5_CUSRE STANDARD; PRT; 135 AA.
AC P4097;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CYTOCHROME B5.
OS Cuscuta reflexa (Southern Asian dodder).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Solanales; Convolvulaceae; Cuscuta.
OX NCBI_TaxID=4129;
RN [1]
RP SEQUENCE FROM N.A.
RP MEDLINE=95047507; PubMed=7959021;
RA Subramaniam K., Mahadevan S.;
RT "The cDNA sequence of cytochrome b5 associated with cytokinin-induced
RT haustoria formation in Cuscuta reflexa."
RL Gene 149:375-376(1994).
CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
CC OXYGENASES.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC -----
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CC EMBL: L22209; AAA62621.1; -
DR HSSP: P04166; 1B5M.
DR InterPro: IPR001199; -
DR Pfam: PF00173; heme_1; 1.
DR PRINTS: PR00363; CYTOCHROME_B5.
DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KW Electron transport; Transmembrane; Heme; Microsome.
FT BINDING 39 39 HEME LIGAND (BY SIMILARITY).
FT BINDING 63 63 HEME LIGAND (BY SIMILARITY).
FT TRANSMEM 106 126 POTENTIAL.
SQ SEQUENCE 135 AA; 14745 MW; CFF2IC932981F5DA CRC64;

Query Match 100.0%; Score 26; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KXYDV 5
DB 28 KXYDV 32

RESULT 7
CYB5_TOBAC STANDARD; PRT; 136 AA.
AC P49098;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CYTOCHROME B5.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=94325476; PubMed=8049375;
RA Smith M.A., Stobart A.K., Shewry P.R., Napier J.A.;
RT Tobacco cytochrome b5: cDNA isolation, expression analysis and in
RT vitro protein targeting.
RT Plant Mol. Biol. 25:527-537(1994).
CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CC OXGENASES. MAY PLAY A KEY ROLE IN THE MODIFICATION BY
CC DESATURATION OF FATTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHICH IN
CC THE DEVELOPING SEED IS UTILIZED FOR MEMBRANE SYNTHESIS AND IN THE
CC DEVELOPMENTALLY REGULATED PRODUCTION OF LARGE AMOUNTS OF STORAGE
CC LIPIDS. IS INVOLVED IN THE REDUCTION OF CYTOCHROME P-450 AND
CC MAY THEREFORE BE INVOLVED IN FLAVONOID BIOSYNTHESIS IN THE PETALS.
CC -1- SUBCELLULAR LOCATION: MICROSOAL MEMBRANE. BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: IS HIGHLY EXPRESSED IN DEVELOPING SEEDS,
CC MODERATELY EXPRESSED IN FLOWERS, AND IS EXPRESSED AT LOW
CC LEVELS IN THE LEAF.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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DR EMBL: X71441; CAA50575.1; ALT_INIT.

DR EMBL: X68140; CAA48240.1; -
DR HSSP: P04166; 1B5M.
DR InterPro: IPR001199; -
DR Pfam: PF00173; heme_1; 1.
DR PRINTS: PR00363; CYTOCHROME_B5.
DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KW Electron transport; Transmembrane; Heme; Microsome; Multigene family.
FT BINDING 40 40 HEME LIGAND (BY SIMILARITY).
FT BINDING 64 64 HEME LIGAND (BY SIMILARITY).
FT TRANSMEM 107 127 POTENTIAL.
FT CONFLICT 10 11 LA -> EF (IN CAA48240).
FT CONFLICT 105 105 MISSING (IN CAA48240).
SQ SEQUENCE 136 AA; 14979 MW; DACE9EA695B2835F CRC64;

Query Match 100.0%; Score 26; DB 1; Length 136;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KXYDV 5
DB 29 KXYDV 33

RESULT 8
YDAL_SCHPO STANDARD; PRT; 274 AA.
ID YDAL_SCHPO
AC Q10343;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HYPOTHETICAL PROTEIN C1F12.01C IN CHROMOSOME I (FRAGMENT).
GN SPAC1F12.01C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA McLean J., Harris D., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
CC SUBUNIT FAMILY.
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CC EMBL: Z69944; CAA93805.1; -
DR InterPro: IPR000644; -
DR Pfam: PF00571; CBS; 3.
KW Hypothetical protein.
FT NON_TER 274 274
SQ SEQUENCE 274 AA; 30643 MW; 0B1B7E97A4CF3724 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 274;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KXYDV 5
DB 203 KXYDV 207

RESULT 9


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TRXB_AQUAE          STANDARD:      PRT:      323 AA.
ID   TRXB_AQUAE
AC   066790;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   THIOREDOXIN REDUCTASE (EC 1.6.4.5) (TRXR).
GN   TRXB OR AQ_500.
OS   Aquifex aeolicus.
OC   Bacteria; Aquificales; Aquificaceae; Aquifex.
OX   NCBI_TaxId=63363;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VF5;
RX   MEDLINE=98196666; PubMed=9537320;
RA   Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA   Graham D.E., Overbeek R., Sneed M.A., Keller M., Ajay M., Huber R.,
RA   Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT   "The complete genome of the hyperthermophilic bacterium Aquifex
RT   aeolicus."
RL   Nature 392:353-358(1998).
CC   -1- CATALYTIC ACTIVITY: NADPH + OXIDIZED THIOREDOXIN = NADP(+) +
CC   REDUCED THIOREDOXIN.
CC   -1- COFACTOR: FAD.
CC   -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC   -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC   -1- MISCELLANEOUS: THE ACTIVE SITE IS A REDOX-ACTIVE DISULFIDE BOND.
CC   -1- SIMILARITY: BELONGS TO THE PYRIDINE NUCLEOTIDE-DISULFIDE
CC   OXIDOREDUCTASES CLASS-II.
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-----
CC   EMBL: AE000693; AAC06756.1; -.
CC   DR   HSSP: P09625; 1TDE.
CC   DR   InterPro: IPR000103; -.
CC   DR   PROSITE: PS00573; PYRIDINE_REDOX_2; FALSE_NEG.
CC   KW   Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD.
CC   FT   NP_BIND      13      28      FAD (ADP PART) (PROBABLE).
CC   FT   DISULFID     143     146     REDOX-ACTIVE (BY SIMILARITY).
CC   FT   NP_BIND      155     169     NAD(P) (BY SIMILARITY).
CC   FT   NP_BIND      276     286     FAD (FLAVIN PART) (BY SIMILARITY).
CC   FT   NP_BIND      323     328     FAD (FLAVIN PART) (BY SIMILARITY).
CC   SQ   SEQUENCE      323 AA; 35101 MW; 363FC62EFD03328 CRC64;

Query Match          100.0%; Score 26; DB 1; Length 323;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY   1 KKYDV 5
DB   11 KKYDV 15

RESULT 10
FLAD_RHIME          STANDARD:      PRT:      395 AA.
ID   FLAD_RHIME
AC   052942;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   FLAGELLIN D.
GN   FLAD.
OS   Rhizobium meliloti (Sinorhizobium meliloti).
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Rhizobiaceae; Sinorhizobium.
OX   NCBI_TaxId=382;
RN   [1]

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RP   SEQUENCE FROM N.A.
RC   STRAIN=RU1/001;
RA   Platzer J., Schmitt R.;
RL   Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
CC   -1- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO
CC   FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
CC   -1- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
-----
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-----
CC   EMBL: L49337; AAB81421.1; -.
CC   DR   InterPro: IPR001029; -.
CC   DR   InterPro: IPR001492; -.
CC   DR   Pfam: PF00700; Flagellin_C; 1.
CC   DR   Pfam: PF00669; Flagellin_N; 1.
CC   KW   Flagella; Multigene family.
CC   SQ   SEQUENCE      395 AA; 40955 MW; FCA87D670B5C96EE CRC64;

Query Match          100.0%; Score 26; DB 1; Length 395;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY   1 KKYDV 5
DB   185 KKYDV 189

RESULT 11
PST_MAIZE          STANDARD:      PRT:      410 AA.
ID   PST_MAIZE
AC   P49085;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   PHYTOENE SYNTHASE PRECURSOR (EC 2.5.1.-).
GN   y1.
OS   Zea mays (maize).
OC   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC   Magnoliophyta; Liliopsida; Poales; Poaceae; Panicoideae;
OC   Andropogoneae; Zea.
OC   NCBI_TaxId=4577;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96304610; PubMed=8722297;
RA   Buckner B., Sammiuel P., Janick-Buckner D., Bennetzen J.L.;
RT   "The y1 gene of maize codes for phytoene synthase."
RL   Genetics 143:479-488(1996).
CC   -1- FUNCTION: CATALYZES THE REACTION FROM PREPHYTOENE DIPHOSPHATE
CC   TO PHYTOENE.
CC   -1- CATALYTIC ACTIVITY: 2 GERANYLGERANYL DIPHOSPHATE = PHYOPHOSPHATE +
CC   PREPHYTOENE DIPHOSPHATE.
CC   -1- CATALYTIC ACTIVITY: PREPHYTOENE DIPHOSPHATE = PHYOPHOSPHATE +
CC   PHYTOENE.
CC   -1- PATHWAY: CAROTENOID BIOSYNTHESIS.
CC   -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC   -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC   -1- SIMILARITY: BELONGS TO THE PHYTOENE/SQUALENE SYNTHETASE FAMILY.
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DR EMBL: U32636; AAB60314.1; -
 DR MaltzDB: 66643; -
 DR InterPro: IPR002060; -
 DR Pfam: PF00494; SOS_PSY.1.
 DR PROSITE: PS01044; SQUALEN_PHYTOEN_SYN_1; 1.
 DR PROSITE: PS01045; SQUALEN_PHYTOEN_SYN_2; 1.
 KM Multifunctional enzyme; Carotenoid biosynthesis;
 KM Isoprene biosynthesis; Transferase; Chloroplast; Transit peptide.
 FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
 FT CHAIN 1 ? PHYTOENE SYNTHASE.
 FT VARIANT 344 344 N->T (IN ALLELE B73).
 SQ SEQUENCE 410 AA: 46481 MW: 21070A33624EED79 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 410;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KYVDV 5
 |||||
 Db 80 KYVDV 84

RESULT 12
 PSY_NARPS STANDARD: PRT; 423 AA.
 ID PSY_NARPS
 AC PS3797;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE PHYTOENE SYNTHASE PRECURSOR (EC 2.5.1.-).
 GN PSY.
 OS Narcissus pseudonarcissus (Daffodil).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae; Narcissus.
 OX NCBI_TaxID=39639;
 RN [1]
 RC SEQUENCE FROM N.A.
 RA Tissue-Paracorralla;
 RA Schledt M., Beyer P.;
 RT "Nucleotide sequence of a Narcissus pseudonarcissus cDNA for phytoene synthase.";
 RL (in) Plant Gene Register PGR95-122.
 CC -1- FUNCTION: CATALYSES THE REACTION FROM PREPHYTOENE DIPHOSPHATE TO PHYTOENE.
 CC -1- CATALYTIC ACTIVITY: 2 GERANYLGERANYL DIPHOSPHATE = PYROPHOSPHATE + PREPHYTOENE DIPHOSPHATE.
 CC -1- CATALYTIC ACTIVITY: PREPHYTOENE DIPHOSPHATE + PHYTOENE.
 CC -1- PATHWAY: CAROTENOID BIOSYNTHESIS.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -1- SIMILARITY: BELONGS TO THE PHYTOENE/SQUALENE SYNTHETASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: X78814; CAA5391.1; -
 DR InterPro: IPR002060; -
 DR Pfam: PF00494; SOS_PSY.1.
 DR PROSITE: PS01044; SQUALEN_PHYTOEN_SYN_1; 1.
 DR PROSITE: PS01045; SQUALEN_PHYTOEN_SYN_2; 1.
 KM Multifunctional enzyme; Carotenoid biosynthesis;
 KM Isoprene biosynthesis; Transferase; Chloroplast; Transit peptide.
 FT TRANSIT 1 136 CHLOROPLAST (POTENTIAL).
 FT CHAIN 137 423 PHYTOENE SYNTHASE.
 SQ SEQUENCE 423 AA: 47805 MW: 8676BA35312B73DF CRC64;

Query Match 100.0%; Score 26; DB 1; Length 423;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KYVDV 5
 |||||
 Db 87 KYVDV 91

RESULT 13
 THDH_ARXAD STANDARD: PRT; 550 AA.
 ID THDH_ARXAD
 AC 042615;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE THREONINE DEHYDRATASE PRECURSOR (EC 4.2.1.16) (THREONINE DEAMINASE).
 GN ILV1.
 OS Arxula adeninivorans.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Dipodascaceae; mitosporic Dipodascaceae; Arxula.
 OX NCBI_TaxID=37620;
 RN [1]
 RC SEQUENCE FROM N.A.
 RA STRAIN-LS3;
 RX MEDLINE=98398049; PubMed=9730281;
 RA Wartmann T., Roessel H., Kunze I., Bode R., Kunze G.;
 RT "Aliv1 gene from the yeast Arxula adeninivorans LS3 -- a new selective transformation marker."
 RL Yeast 14:1017-1025(1998).
 CC -1- CATALYTIC ACTIVITY: L-THREONINE + H(2)O = 2-OXOBUTANOATE + NH(3) + H(2)O.
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
 CC -1- PATHWAY: FIRST STEP OF ISOLEUCINE BIOSYNTHESIS.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
 CC -1- SIMILARITY: TO THREONINE DEHYDRATASE CATABOLIC AND SERINE DEHYDRATASE.
 CC -----
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 CC -----
 CC EMBL: AJ222772; CAA10977.1; -
 DR InterPro: IPR00634; -
 DR InterPro: IPR001721; -
 DR InterPro: IPR001926; -
 DR Pfam: PF00291; S.T.dehydratase; 1.
 DR Pfam: PF00585; Thr_dehydrat_C; 2.
 DR PROSITE: PS00165; DEHYDRATASE_SER_THR; 1.
 KM Isoleucine biosynthesis; Lyase; Mitochondrion; Pyridoxal phosphate;
 KM Transit peptide.
 FT TRANSIT 1 ? MITOCHONDRION (POTENTIAL).
 FT CHAIN 1 550 THREONINE DEHYDRATASE.
 FT BINDING 86 86 PYRIDOXAL PHOSPHATE.
 SQ SEQUENCE 550 AA: 60416 MW: D08CE5BD55C8A6F CRC64;

Query Match 100.0%; Score 26; DB 1; Length 550;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KYVDV 5
 |||||
 Db 48 KYVDV 52

RESULT 14

DPOL_APPRD
ID DPOL_APPRD STANDARD: PRT; 553 AA.
AC P10479;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE DNA POLYMERASE (EC 2.7.7.7) (PROTEIN P1).
GN 1.
OS Bacteriophage PRD1.
OC Viruses; dsDNA viruses, no RNA stage; Tectiviridae; Tectivirus.
OX NCBI_TaxID=10658;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=88068579; PubMed=3479792;
RX Jung G., Leavitt M.C., Hsieh J.-C., Ito J.;
RT "Bacteriophage PRD1 DNA polymerase: evolution of DNA polymerases.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:8287-8291(1987).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=88112855; PubMed=3322943;
RX Savillahi H., Bamford D.H.;
RT "The complete nucleotide sequence of the left very early region of Escherichia coli bacteriophage PRD1 coding for the terminal protein and the DNA polymerase.";
RL Gene 57:121-130(1987).
RN [3]
RP SEQUENCE OF 1-9 FROM N.A.
RA MEDLINE=88067710; PubMed=3684578;
RX Hsieh J.-C., Jung G., Leavitt M.C., Ito J.;
RT "Primary structure of the DNA terminal protein of bacteriophage PRD1.";
RL Nucleic Acids Res. 15:8999-9009(1987).
RN [4]
RP MUTAGENESIS.
RX MEDLINE=90358833; PubMed=2202298;
RT Jung G., Leavitt M.C., Schultz M., Ito J.;
RT Site-specific mutagenesis of PRD1 DNA polymerase: mutations in highly conserved regions of the family B DNA polymerase.";
RL Biochem. Biophys. Res. Commun. 170:1294-1300(1990).
CC -1- FUNCTION: THIS POLYMERASE POSSESSES TWO ENZYMOLOGIC ACTIVITIES: DNA SYNTHESIS (POLYMERASE) AND AN EXONUCLEOTIC ACTIVITY THAT DEGRADES SINGLE STRANDED DNA IN THE 3' TO 5' DIRECTION.
CC -1- CATALYTIC ACTIVITY: N-DEOXYNUCLEOSIDE TRIPHOSPHATE -
CC N PYROPHOSPHATE + DNA(N).
CC -1- MISCELLANEOUS: THIS DNA POLYMERASE REQUIRES A PROTEIN AS A PRIMER.
CC -1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
CC -----
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CC -----
DR EMBL: M69077; AAA32456.1; -
DR EMBL: J03018; AAA32452.1; -
DR EMBL: M22161; AAA32450.1; -
DR EMBL: X06321; CAA29637.1; -
DR PIR: B27328; DIBPOL.
DR PIR: A39970; A39970.
DR InterPro: IPR002064; -
DR PRINTS: PR00106; DNAPOL.
DR PROSITE: PS00116; DNA_POLYMERASE_B; 1.
KM Transferase: DNA-directed DNA polymerase; DNA replication;
KW DNA-binding; Hydrolyase; Exonuclease.
FT DOMAIN 1 7210 3-5' EXONUCLEASE ACTIVITY.
FT DOMAIN 7211 553 POLYMERASE ACTIVITY.
SQ SEQUENCE 553 AA; 63336 MW; 65E61D059BDD51E CRC64;

Query Match 100.0%; Score 26; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDV 5
|||||
Db 217 KVDV 221
RESULT 15
ID PEPI_LACLA STANDARD: PRT; 601 AA.
AC P54124; P94880;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE OLIGONUCLEOTIDASE F, PLASMID (EC 3.4.24.-).
GN PEPEP OR PEPE.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OG Plasmid pUP763.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=NCDO 763;
RX MEDLINE=95096044; PubMed=7798200;
RA Monnet V., Nardi M., Chopin A., Chopin M.-C., Gripon J.-C.;
RT "Biochemical and genetic characterization of PepF, an oligopeptidase from Lactococcus lactis.";
RL J. Biol. Chem. 269:32070-32076(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NCDO 763;
RX MEDLINE=97352670; PubMed=9209029;
RA Nardi M., Renault P., Monnet V.;
RT "Duplication of the pepF gene and shuffling of DNA fragments on the lactose plasmid of Lactococcus lactis.";
RL J. Bacteriol. 179:4164-4171(1997).
CC -1- FUNCTION: HYDROLYSES PEPTIDES CONTAINING BETWEEN 7 AND 17 AMINO ACIDS WITH A RATHER WIDE SPECIFICITY.
CC -1- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3 (ZINC METALLOPROTEASE); ALSO KNOWN AS THE THIMET OLIGOPEPTIDASE SUBFAMILY.
CC -----
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CC -----
DR EMBL: Z32522; CAA83534.1; -
DR EMBL: X99798; CAA68133.1; -
DR MEROPS: M03.007; -
DR InterPro: IPR00130; -
DR InterPro: IPR001567; -
DR Pfam: PF01432; Peptidase_M3; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; FALSE NEG.
KM Hydrolyase; Metalloprotease; Zinc; Plasmid.
FT METAL 387 388
FT ACT_SITE 388 388
FT METAL 391 391
FT METAL 394 394
FT METAL 394 394
FT CONFLICT 518 518
FT CONFLICT 518 518
SQ SEQUENCE 601 AA; 69674 MW; C8B5C519FAAF787 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVDV 5
|||||

Db 266 KVDV 270

Search completed: August 9, 2001, 20:36:49
Job time: 698 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 9, 2001, 20:26:04 ; Search time 50.69 Seconds

(without alignments)
7.514 Million cell updates/sec

Title: US-09-367-013b-2_COPY_39_43

Perfect score: 26

Sequence: 1 KVVYDV 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_68:*

2: PIR1:*

3: PIR2:*

4: PIR3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	51	2 P00816	probable cytochrom
2	26	100.0	89	2 D64414	hypothetical prote
3	26	100.0	120	2 S63052	cytochrome b5 - ye
4	26	100.0	124	2 T40071	cytochrome b5 - fl
5	26	100.0	134	2 T52469	cytochrome b5 (imp
6	26	100.0	134	2 T14454	cytochrome b5 - w1
7	26	100.0	135	2 A86390	hypothetical prote
8	26	100.0	135	2 T09946	cytochrome b5 - so
9	26	100.0	139	2 S46306	cytochrome b5 - co
10	26	100.0	140	2 T52468	cytochrome b5 (imp
11	26	100.0	141	2 T15210	probable cytochrom
12	26	100.0	151	2 G84425	hypothetical prote
13	26	100.0	151	2 T05600	probable major lat
14	26	100.0	155	2 S71257	major latex protei
15	26	100.0	263	2 T19387	hypothetical prote
16	26	100.0	274	2 S67444	probable 5'-AMP-ac
17	26	100.0	303	2 E83939	myo-inositol catab
18	26	100.0	313	2 T22116	hypothetical prote
19	26	100.0	315	2 C84096	thioredoxin reduct
20	26	100.0	315	2 H70350	ADP-heptose syntha
21	26	100.0	323	2 B70345	thioredoxin reduct
22	26	100.0	334	2 A86870	oxidoreductase yud
23	26	100.0	355	2 JN0746	site-specific DNA
24	26	100.0	377	2 T50563	beta-1,3-glucanase
25	26	100.0	397	2 H86754	prophage p12 prote
26	26	100.0	410	2 S68307	phytoene synthase
27	26	100.0	423	2 S54135	phytoene synthase
28	26	100.0	449	2 A84900	hypothetical prote
29	26	100.0	449	2 T50555	delta-8 sphingolip

30	26	100.0	454	2 F72589	hypothetical prote
31	26	100.0	516	2 E84019	methylenalonyl-CoA
32	26	100.0	553	1 DJBPD1	DNA-directed DNA P
33	26	100.0	581	2 S44896	ZK1236.1 protein -
34	26	100.0	601	1 A55485	oligopeptidase (EC
35	26	100.0	601	2 G86840	oligendopeptidase
36	26	100.0	634	2 S28724	conserved hypochet
37	26	100.0	686	2 A75126	hypothetical prote
38	26	100.0	701	2 D83677	hypothetical prote
39	26	100.0	738	2 D70680	hypothetical prote
40	26	100.0	805	1 A55054	calpain (EC 3.4.22
41	26	100.0	805	2 PL0034	photosystem I chal
42	25	96.2	98	2 T41691	hypothetical prote
43	25	96.2	113	2 T41691	prophage p11 prote
44	25	96.2	120	2 C86681	probable Cytochrom
45	25	96.2	121	2 H96631	conserved hypochet
			123	2 G72032	

ALIGNMENTS

RESULT 1
PQ0816
Probable cytochrome b5 - rape (fragment)
C:Species: Brassica napus (rape)
C:Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 20-Apr-2000
C:Accession: PQ0816
R:Park, Y.S.; Kwak, J.M.; Kwon, O.Y.; Klm, Y.S.; Lee, D.S.; Cho, M.J.; Lee, H.H.; Nam
Plant Physiol. 103, 359-370, 1993
A:Title: Generation of expressed sequence tags of random root cDNA clones of Brassica
A:Reference number: PQ0816; MUID:94302145
A:Accession: PQ0816
A:Molecule type: mRNA
A:Residues: 1-51 <PAR>
A:Experimental source: root, cv. Naehan
C:Superfamily: cytochrome b5; cytochrome b5 core homology (fragment) <CB5>
F:1-51/Domain: cytochrome b5 core homology (fragment) <CB5>

Query Match 100.0%; Score 26; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVYDV 5
Db 2 KVVYDV 6

RESULT 2

D64414
Hypothetical protein MJ0916 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Sep-1996
C:Accession: D64414
R:Balt, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak
Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weissbrock, K.G.; Merrick, J.M.; Glodek,
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc
A:Reference number: A64300; MUID:96337999
A:Accession: D64414
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-89 <BUL>
A:Cross-references: GB:U67535; GB:L77117; NTD:G1591586; PID:G1591589; TIGR:MC0916; PI
C:Genetics:
A:Map position: REV847877-847608
C:Superfamily: hypothetical protein MJ0916

Query Match 100.0%; Score 26; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 36;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYVDV 5
|||||

Db 23 KYVDV 27

RESULT 3

S63052
cytochrome b5 - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein N1949; protein YNL111C
C:Species: Saccharomyces cerevisiae
C>Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 20-Jun-2000
C:Accession: S63052; S47919; S67347
R:De Antoni, A.; D'Angelo, M.; Dal Pero, F.; Sartorello, F.; Pandolfo, D.; Lanfranchi, C.
submitted to the Protein Sequence database, April 1996
A:Reference number: S63047
A:Accession: S63052
A:Molecule type: DNA
A:Residues: 1-120 <DEA>
A:Cross-references: EMBL:Z71387; NID:q1302031; PIDN:CAA95990.1; PID:q1302032; MIPS:YNL111
A:Experimental source: strain 5288C
R:Truan, G.; Epinat, J.C.; Rougeulle, C.; Cullin, C.; Pompon, D.
Gene 149, 123-127, 1994
A:Title: Cloning and characterization of a yeast cytochrome b(5)-encoding gene which sup
A:Reference number: S47919; MUID:95047457
A:Accession: S47919
A:Molecule type: DNA
A:Residues: 1-16, 'Q', 18-120 <TRU>
A:Cross-references: EMBL:L22494; NID:q431761; PIDN:AAA67468.1; PID:q431762
R:d'Antoni, A.; d'Angelo, M.; dal Pero, F.; Sartorello, F.; Pandolfo, D.; Lanfranchi, G.
submitted to the EMBL Data Library, February 1996
A:Description: The DNA sequence of cosmid 14-13b from chromosome XIV of Saccharomyces ce
A:Reference number: S67327
A:Accession: S67347
A:Molecule type: DNA
A:Residues: 1-120 <DAN>
A:Cross-references: EMBL:Z69382; NID:q1183941; PIDN:CAA93396.1; PID:q1183962
C:Genetics:
A:Gene: SGD:CYB5
A:Cross-references: SGD:S0005055; MIPS:YNL111C
A:Map position: 14L
C:Function:
A:Description: electron transfer
C:Superfamily: cytochrome b5; cytochrome b5 core homology
C:Keywords: electron transfer; heme; iron; metalloprotein; transmembrane protein
F:2-77/Domain: cytochrome b5 core homology <CB5>
F:102-118/Domain: transmembrane #status predicted <TM>
F:37,61/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 100.0%; Score 26; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYVDV 5
|||||

Db 26 KYVDV 30

RESULT 4

T40071
cytochrome b5 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
C:Accession: T40071
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Leleure, V.; Galibert, F.
submitted to the EMBL Data Library, December 1998
A:Reference number: Z21903
A:Accession: T40071
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-124 <LYN>

A:Cross-references: EMBL:AL034463; PIDN:CAA22444.1; GSPDB:GN00067; SPDB:SPBC29A10.16C
A:Experimental source: strain 972h-; cosmid c29A10
C:Genetics:
A:Gene: SPDB:SPBC29A10.16C
A:Map position: 2
A:Introns: 50/1; 101/2
C:Superfamily: cytochrome b5; cytochrome b5 core homology
C:Keywords: heme; iron; metalloprotein
F:38,62/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 100.0%; Score 26; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYVDV 5
|||||

Db 27 KYVDV 31

RESULT 5

T52469
cytochrome b5 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 01-Dec-2000
C:Accession: T52469
R:Fukuchi-Mizutani, M.; Mizutani, M.; Tanaka, Y.; Kusumi, T.; Ohta, D.
Plant Physiol. 119, 353-361, 1999
A:Title: Microsomal Electron Transfer in Higher Plants: Cloning and Heterologous Expr
A:Reference number: Z52474
A:Accession: T52469
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-134 <FUK>
A:Cross-references: EMBL:AB007801; PIDN:CAB17231.1
C:Superfamily: cytochrome b5; cytochrome b5 core homology
C:Keywords: heme; iron; metalloprotein
F:40,64/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 100.0%; Score 26; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYVDV 5
|||||

Db 29 KYVDV 33

RESULT 6

T14454
cytochrome b5 - wild cabbage
C:Species: Brassica oleracea (wild cabbage)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
C:Accession: T14454
R:Kearns, E.V.; Keck, P.; Somerville, C.R.
submitted to the EMBL Data Library, March 1992
A:Description: Nucleotide sequence of cDNA for cytochrome b5 from cauliflower (Brassi
A:Reference number: Z18100
A:Accession: T14454
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-134 <KEA>
A:Cross-references: EMBL:M87514; NID:q167139; PID:q167140
C:Function:
A:Description: acts as electron carrier for membrane-bound oxygenases
C:Superfamily: cytochrome b5; cytochrome b5 core homology
C:Keywords: electron transfer; heme; iron; membrane protein; metalloprotein
F:5-80/Domain: cytochrome b5 core homology <CB5>
F:40,64/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 100.0%; Score 26; DB 2; Length 134;

Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDV 5
|||||
Db 29 KVDV 33

RESULT 7

A66390
hypothetical protein AAF98581.1 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: A66390
R:Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A66141; MUID:21016719
A:Accession: A66390
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-135 <STO>
A:Cross-references: GB:AE005172; NID:99797763; PIDN:AAF98581.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1
C:Superfamily: cytochrome b5; cytochrome b5 core homology

Query Match 100.0%; Score 26; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDV 5
|||||
Db 29 KVDV 33

RESULT 8

T09946
cytochrome b5 - southern Asian dodder
C:Species: Cuscuta reflexa (southern Asian dodder)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T09946
R:Subramaniam, K.; Mahadevan, S.
Gene 149, 375-376, 1994
A:Title: The cDNA sequence of cytochrome b5 associated with cytokinin-induced haustoria
A:Reference number: Z16903; MUID:95047507
A:Accession: T09946
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-135 <SUB>
A:Cross-references: EMBL:L22209; NID:9450584; PIDN:AAA62621.1; PID:9450585
C:Function:
A:Description: acts as electron carrier for membrane-bound oxygenases
C:Superfamily: cytochrome b5; cytochrome b5 core homology
C:Keywords: electron transfer; heme; iron; membrane protein; metalloprotein
F:4-7g/Domain: cytochrome b5 core homology <CB5>
F:39,63/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 100.0%; Score 26; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDV 5
|||||

Db 28 KVDV 32

RESULT 9

S46306
cytochrome b5 - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 05-May-2000
C:Accession: S46306; S33157
R:Smith, M.A.; Stobart, A.K.; Shewry, P.R.; Napier, J.A.
Plant Mol. Biol. 25, 527-537, 1994
A:Title: Tobacco cytochrome b(3): cDNA isolation, expression analysis and in vitro pr
A:Reference number: S46306; MUID:94325476
A:Accession: S46306
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-139 <SMIT>
A:Cross-references: EMBL:X71441; NID:9296385; PIDN:CAA50575.1; PID:9296386
C:Superfamily: cytochrome b5; cytochrome b5 core homology
C:Keywords: heme; iron; metalloprotein
F:8-83/Domain: cytochrome b5 core homology <CB5>
F:43,67/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 100.0%; Score 26; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDV 5
|||||
Db 32 KVDV 36

RESULT 10

T52468
cytochrome b5 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 01-Dec-2000
C:Accession: T52468
R:Fukuchi-Mizutani, M.; Mizutani, M.; Tanaka, Y.; Kusumi, T.; Ohta, D.
Plant Physiol. 119, 353-361, 1999
A:Title: Mitochondrial Electron Transfer in Higher Plants: Cloning and Heterologous Expr
A:Reference number: Z25274
A:Accession: T52468
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-140 <FOK>
A:Cross-references: EMBL:AB007802; PIDN:CAB17232.1
C:Superfamily: cytochrome b5; cytochrome b5 core homology
C:Keywords: heme; iron; metalloprotein
F:40,64/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 100.0%; Score 26; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDV 5
|||||
Db 29 KVDV 33

RESULT 11

T15210
probable cytochrome b5 W02D3.1 [similarity] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
C:Accession: T15210
R:Le, T.; Weinstock, L.; Rikkin, L.
submitted to the EMBL Data Library, May 1997
A:Description: The sequence of C. elegans cosmid W02D3.
A:Reference number: Z18308
A:Accession: T15210

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-141 <LET>
A:Cross-references: EMBL:AF003141; NID:q2088732; PID:q2088733; PIDN:AB54174.1; GSPDB:GN
A:Experimental source: strain Bristol N2; clone W02D3
C:Genetics:
A:Gene: CESP:W02D3.1
A:Map position: 1
A:Introns: 31/3
C:Superfamily: cytochrome b5; cytochrome b5 core homology
C:Keywords: heme; iron; metalloprotein
F:4-82/Domain: cytochrome b5 core homology <CB5>
F:42,66/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 100.0%; Score 26; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KYVDV 5
|||||
DB 31 KYVDV 35

RESULT 12
G84425
hypothetical protein At2g01520 (imported) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: G84425
R:Lin. X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Beutlo, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
Eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: G84425
A:Molecule type: DNA
A:Status: preliminary
A:Cross-references: GB:AE002093; NID:q3785981; PIDN:AC67328.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g01520
A:Map position: 2
C:Superfamily: wound-induced protein Sn-1

Query Match 100.0%; Score 26; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KYVDV 5
|||||
DB 96 KYVDV 100

RESULT 13
T05600
probable major latex protein F9D16.150 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 24-Nov-1999
C:Accession: T05600
R:Bayan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hobeisel, J.; Mewes, H.W.; Meyer, K.F.
submitted to the Protein Sequence Database, February 1999
A:Reference number: Z15419
A:Accession: T05600
A:Molecule type: DNA
A:Residues: 1-151 <BEV>
A:Cross-references: EMBL:AL035394
C:Genetics:
A:Map position: 4
A:Introns: 63/1

A:Note: F9D16.150
C:Superfamily: wound-induced protein Sn-1

Query Match 100.0%; Score 26; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KYVDV 5
|||||
DB 96 KYVDV 100

RESULT 14
S71257
major latex protein type 1 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000
C:Accession: S71257
R:Grellet, F.; Cooke, R.; Laudie, M.; Raynal, M.; Delseny, M.
submitted to the EMBL Data Library, October 1995
A:Reference number: S71257
A:Accession: S71257
A:Molecule type: mRNA
A:Residues: 1-155 <GRE>
A:Cross-references: EMBL:X91960; NID:q1107492; PID:q1107493
C:Superfamily: wound-induced protein Sn-1

Query Match 100.0%; Score 26; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KYVDV 5
|||||
DB 96 KYVDV 100

RESULT 15
T19387
hypothetical protein C18D11.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T19387
R:Barlow, K.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19118
A:Accession: T19387
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-263 <MIT>
A:Cross-references: EMBL:Z92826; PIDN:CA807320.1; GSPDB:GN00021; CESP:C18D11.1
A:Experimental source: clone C18D11
C:Genetics:
A:Gene: CESP:C18D11.1
A:Map position: 3
A:Introns: 28/3; 106/1; 185/3; 210/3

Query Match 100.0%; Score 26; DB 2; Length 263;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KYVDV 5
|||||
DB 209 KYVDV 213

Search completed: August 9, 2001, 20:26:05
Job time: 244 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 9, 2001, 20:36:15 ; Search time 87.05 Seconds
(without alignments)
7.599 Million cell updates/sec

Title: US-09-367-013b-2_COPY_39_43
Perfect score: 26
Sequence: 1 KVDV 5

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: SP_TREMBL_16:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhnc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_unclassified:*
14: sp_vertebrate:*
15: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	51	09S993	Q9S993 brassica na
2	26	100.0	117	09W419	Q9W419 drosophila
3	26	100.0	124	09A391	Q9A391 schizosacch
4	26	100.0	128	09B634	Q9B634 bacterioph
5	26	100.0	132	024651	Q24651 olea europa
6	26	100.0	134	048618	Q48618 olea europa
7	26	100.0	135	09GV21	Q9GV21 polyanthra
8	26	100.0	135	10	Q9EDW8
9	26	100.0	140	10	Q9ZWT2
10	26	100.0	141	5	001816
11	26	100.0	142	2	066353
12	26	100.0	151	10	Q9ZVF3
13	26	100.0	151	10	Q9SUQ9
14	26	100.0	155	2	082979
15	26	100.0	155	10	Q39132
16	26	100.0	212	5	Q9V6K5
17	26	100.0	212	5	Q9NAK3
18	26	100.0	254	5	Q9X148
19	26	100.0	263	5	Q9XTZ4

20	26	100.0	303	2	Q9KAH0	Q9KAH0 bacillus ha
21	26	100.0	313	5	Q20355	Q20355 caenorhabd1
22	26	100.0	315	2	Q66836	Q66836 aquilex aeo
23	26	100.0	315	2	Q9K703	Q9K703 bacillus ha
24	26	100.0	377	10	Q9ZNV6	Q9ZNV6 oryza sativ
25	26	100.0	448	10	Q9MBD4	Q9MBD4 petunia hyb
26	26	100.0	449	10	Q82348	Q82348 arabidopsi
27	26	100.0	449	10	Q9ZRP8	Q9ZRP8 arabidopsi
28	26	100.0	454	1	Q9YCS5	Q9YCS5 aeropyrum p
29	26	100.0	457	3	Q9UYV3	Q9UYV3 mortierella
30	26	100.0	457	3	Q9UYV3	Q9UYV3 mortierella
31	26	100.0	457	3	Q9HEY4	Q9HEY4 mortierella
32	26	100.0	457	3	Q9HEY1	Q9HEY1 mortierella
33	26	100.0	471	10	Q9FLP4	Q9FLP4 arabidopsi
34	26	100.0	516	2	Q9KBP6	Q9KBP6 bacillus ha
35	26	100.0	520	10	Q9LEM9	Q9LEM9 ceratodon p
36	26	100.0	525	10	Q9ZNM2	Q9ZNM2 physcomitre
37	26	100.0	561	10	Q9LQ77	Q9LQ77 arabidopsi
38	26	100.0	634	1	Q50838	Q50838 methanococc
39	26	100.0	635	5	Q9GNQ7	Q9GNQ7 leishmania
40	26	100.0	686	1	Q9V011	Q9V011 pyrococcus
41	26	100.0	701	2	Q9KQ92	Q9KQ92 bacillus ha
42	26	100.0	729	2	Q9E168	Q9E168 vibrio harv
43	26	100.0	729	2	Q9E154	Q9E154 vibrio sp.
44	26	100.0	768	13	Q9W750	Q9W750 anguilla an
45	26	100.0	828	5	Q9V8U7	Q9V8U7 drosophila

ALIGNMENTS

RESULT 1
ID 09S993 PRELIMINARY: PRT: 51 AA.

AC 09S993; 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CYTOCHROME B5 HOMOLOG (FRAGMENT).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94302145; PubMed=8029332;
RA Park Y.S., Kwak J.M., Kwon O.Y., Kim Y.S., Lee D.S., Cho M.J.,
RA Lee H.H., Nam H.G.;
RT "Generation of expressed sequence tags of random root cDNA clones of
RT Brassica napus by single-run partial sequencing."
RL Plant Physiol. 103:359-370(1993).
CC -1 SIMILARITY: TO CYTOCHROME B5 DOMAIN.
DR HSP; P04166; 1BSM.
DR InterPro; IPR001199; .
DR Pfam; PF00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROME B5.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 51 AA: 5609 MW: 4A0472174876B020 CRC64;

Query Match 100.0%; Score 26; DB 10; Length 51;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDV 5
|||||
Db 2 KVDV 6

RESULT 2
Q9WA19

ID Q9W419 PRELIMINARY; PRT; 117 AA.
AC Q9W419;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE CG3566 PROTEIN.
GN CG3566.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Chamee M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Abdayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borisy D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durkin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jallat M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacble J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveril J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT *The genome sequence of Drosophila melanogaster.*;
RL Science 287:2185-2195(2000).
CC -1- SIMILARITY: TO CYTOCHROME B5 DOMAIN.
DR EMBL: AE003437; AAF46141.1; -;
DR HSSP: P04166; 1BSM.
DR FLYBASE: FBgn0029854; CG3566.
DR InterPro: IPR001199; -;
DR Pfam: PF00173; heme_1; 1.
DR PRINTS: PR00363; CYTOCHROME5.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 117 AA; 12942 MW; BBAF111D4FC8022 CRC64;

Query Match 100.0%; Score 26; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYVDV 5
26 KYVDV 30

RESULT 3
ID Q94391 PRELIMINARY; PRT; 124 AA.
AC Q94391;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE PROBABLE CYTOCHROME B5.
GN SPC29A10.16C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
NCBI_TaxID=4896;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-972;
RA Lyne M., Rajandream M.A., Barrell B.G., Lelaire V., Galibert F.,
Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CC -1- FUNCTION: AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
CC OXYGENASES.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
DR EMBL: AF034463; CA22444.1; -;
DR InterPro: IPR001199; -;
DR Pfam: PF00173; heme_1; 1.
DR PRINTS: PR00363; CYTOCHROME5.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KW Hypothetical protein; Electron transport; Transmembrane; Heme;
KW Microsome.
FT BINDING 38 38 HEME LIGAND (BY SIMILARITY).
FT BINDING 62 62 HEME LIGAND (BY SIMILARITY).
FT TRANSMEM 100 120 POTENTIAL.
SQ SEQUENCE 124 AA; 13910 MW; 299D12CB693831D4 CRC64;

Query Match 100.0%; Score 26; DB 3; Length 124;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYVDV 5
27 KYVDV 31

RESULT 4
ID Q38634 PRELIMINARY; PRT; 128 AA.
AC Q38634;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-NOV-1996 (TREMBLrel. 01, last annotation update)
DE FRD2.
GN FRD2.
OS Bacteriophage L26, and Bacteriophage L21.
OC Viruses.
NCBI_TaxID=42177, 42175;
RN (1)
RP SEQUENCE FROM N.A.
RA Pogozhov A.B., Porter D., Kutter E.M., Mesyanzhinov V.V.;
Submitted (OCT-1995) to the EMBL/Genbank/DBJ databases.
DR EMBL: L46838; AAA74682.1; -;
DR EMBL: L46834; AAA74674.1; -;
SQ SEQUENCE 128 AA; 14871 MW; EFP9F7F1F8893CE14 CRC64;

Query Match 100.0%; Score 26; DB 9; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDV 5
 |||||
 Db 99 KVDV 103

RESULT 5
 024651 PRELIMINARY; PRT; 132 AA.

AC 024651;
 DT 01-JAN-1998 (TEMBLrel. 05, Created)
 DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
 DE 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
 DE CYTOCHROME B5 (FRAGMENT).
 GN CYTB5-1.
 OS Olea europaea (Common olive).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
 OC Lamiales; Oleaceae; Olea.
 NCBI_TaxID=4146;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. KORONEIKI;
 RA Martinkovskaya A.I., Poghosyan Z.P., Haralambidis K.G.,
 RA Hatzipoulos P., Murphy D.J.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO CYTOCHROME B5 DOMAIN.
 DR HSSP: P001369; CAA04702.1; -.
 DR EMBL: AJ001369; CAA04702.1; -.
 DR HSSP: P00171; 1MDB.
 DR Mendel: 24387; Olea,1218;24387.
 DR InterPro: IPR001199; -.
 DR Pfam: PF00173; heme_1; 1.
 DR PRINTS: PR00363; CYTOCHROME_B5.
 DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 FT NON_TER 1 1
 SQ SEQUENCE 132 AA; 14683 MW; 4D84FA0C3662DA83 CRC64;

Query Match 100.0%; Score 26; DB 10; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDV 5
 |||||
 Db 26 KVDV 30

RESULT 6
 048618 PRELIMINARY; PRT; 134 AA.

AC 048618;
 DT 01-JUN-1998 (TEMBLrel. 06, Created)
 DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
 DE 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
 DE CYTOCHROME B5 (FRAGMENT).
 GN CYTB5-2.
 OS Olea europaea (Common olive).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
 OC Lamiales; Oleaceae; Olea.
 NCBI_TaxID=4146;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. KORONEIKI;
 RA Martinkovskaya A.I.;
 RA Hatzipoulos P., Murphy D.J.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO CYTOCHROME B5 DOMAIN.
 DR HSSP: P001369; CAA04702.1; -.
 DR EMBL: AJ001369; CAA04702.1; -.
 DR HSSP: P00171; 1MDB.
 DR Mendel: 24387; Olea,1218;24387.
 DR InterPro: IPR001199; -.
 DR Pfam: PF00173; heme_1; 1.
 DR PRINTS: PR00363; CYTOCHROME_B5.
 DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 FT NON_TER 1 1
 SQ SEQUENCE 132 AA; 14683 MW; 4D84FA0C3662DA83 CRC64;

CC -1- SIMILARITY: TO CYTOCHROME B5 DOMAIN.
 DR EMBL: AJ001370; CAA04703.1; -.
 DR HSSP: P04166; 1B5M.
 DR Mendel: 27871; Olea,1218;27871.
 DR InterPro: IPR001199; -.
 DR Pfam: PF00173; heme_1; 1.
 DR PRINTS: PR00363; CYTOCHROME_B5.
 DR PROSITE: PS00191; CYTOCHROME_B5_1; UNKNOWN_1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 FT NON_TER 1 1
 SQ SEQUENCE 134 AA; 15316 MW; 8DFC02C59516322D CRC64;

Query Match 100.0%; Score 26; DB 10; Length 134;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDV 5
 |||||
 Db 29 KVDV 33

RESULT 7
 09GV21 PRELIMINARY; PRT; 135 AA.

AC 09GV21;
 DT 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
 DE 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
 DE CYTOCHROME B5.
 GN PMCYTB5.
 OS Polyandrocampa misakiensis.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
 OC Stolidobranchia; Scyliidae; Polyandrocampa.
 NCBI_TaxID=7723;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yubisui T., Takahashi F., Takabayashi T., Fujiwara S., Kawamura K.;
 RT "Nucleotide sequence of cytochrome b5 cDNA of Polyandrocampa
 misakiensis and characterization of recombinant protein."
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB042613; BAB17853.1; -.
 SQ SEQUENCE 135 AA; 15465 MW; 3E63ACF42BF7EE1 CRC64;

Query Match 100.0%; Score 26; DB 5; Length 135;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDV 5
 |||||
 Db 35 KVDV 39

RESULT 8
 09FDW8 PRELIMINARY; PRT; 135 AA.

AC 09FDW8;
 DT 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
 DE 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
 DE PUTATIVE CYTOCHROME B5 PROTEIN (TIK7.28 PROTEIN).
 GN TIK7.28.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Etgu P., Lee J.M.,
 Toriumi M., Yu G., Brooks S., Chao Q., Chen H., Karlin-Neumann G.,

RA Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shin P.,
 RA Southwick A., Davis R.W., Ecker J.R., Theologis A.;
 RT "Full length cDNA of gene TIK7.28 (GI:9797763)";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Sakano H., Liu S.X., Yu G., Lee J.M., Lenz C., Pham P., Toriumi M.,
 RA Chin C., Chlou J., Choi E., Chung M., Gonzalez A., Howng B., Liu A.,
 RA Vaysberg M., Altfati H., Brooks S., Buehler E., Chao Q., Conn L.,
 RA Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B.,
 RA Miranda M., Nguyen M., Palm C.J., Shin P., Southwick A., Davis R.W.,
 RA Ecker J.R., Federpsiel N.A., Theologis A.;
 RT "The sequence of BAC TIK7 from Arabidopsis thaliana chromosome 1.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF332415; AAC48778.1; -;
 DR EMBL: AC013427; AAF95581.1; -;
 SQ SEQUENCE 135 AA; 15220 MW; F88FCB6B5BEC8E9E CRC64;

Query Match 100.0%; Score 26; DB 10; Length 135;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVVYD 5
 Db 29 KVVYD 33

RESULT 9
 ID 09ZWT2 PRELIMINARY; PRT; 140 AA.
 AC 09ZWT2;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE CYTOCHROME B5.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxId=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99097071; PubMed=9880378;
 RA Fukuchi-Mizutani M., Mizutani M., Tanaka Y., Kusumi T., Ohta D.,
 RT "Microsomal electron transfer in higher plants: cloning and
 RT heterologous expression of NADH-cytochrome b5a reductase from
 RT Arabidopsis.";
 RL Plant Physiol. 119:353-361(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA MEDLINE=98403884; PubMed=9734815;
 RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
 RT Sequence features of the regions of 1,367,185 bp covered by 19
 RT physically assigned P1 and TAC clones.";
 RL DNA Res. 5:203-216(1998).
 CC -1- SIMILARITY: TO CYTOCHROME B5 DOMAIN.
 DR EMBL: AB007802; CAB17232.1; -;
 DR EMBL: AB012442; BAB0934.1; -;
 DR HSSP: P04166; 1B5M.
 DR Mendel: 34947; Arabid.1218;34947.
 DR InterPro: IPR001199; -;
 DR Pfam: PF00173; heme_1; 1.
 DR PRINTS: PRO0363; CYTOCHROME_B5.
 DR PROSITE: PS00191; CYTOCHROME_B5_1; UNKNOWN_1.
 DR PROSITE: PS0255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 140 AA; 15097 MW; 18C24F8F7995E08 CRC64;

Query Match 100.0%; Score 26; DB 10; Length 140;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVVYD 5
 Db 29 KVVYD 33

RESULT 10
 ID 001816 PRELIMINARY; PRT; 141 AA.
 AC 001816;
 DT 01-JUL-1997 (TREMblrel. 04, Created)
 DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE SIMILAR TO CYTOCHROME B5.
 GN W02D3.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxId=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey J., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
 RA Smailton N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Le T., Weinstock L., Rifkin L.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO CYTOCHROME B5 DOMAIN.
 DR EMBL: AF003141; AAB54174.1; -;
 DR HSSP: P04166; 1B5M.
 DR InterPro: IPR001199; -;
 DR Pfam: PF00173; heme_1; 1.
 DR PROSITE: PS00191; CYTOCHROME_B5_1; UNKNOWN_1.
 DR PROSITE: PS0255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 141 AA; 15633 MW; AD1AF60BD69F3A5 CRC64;

Query Match 100.0%; Score 26; DB 5; Length 141;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVVYD 5
 Db 31 KVVYD 35

RESULT 11
 ID 066353 PRELIMINARY; PRT; 142 AA.

AC 066353;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE ALPHA SUBUNIT OF DINITROGENASE REDUCTASE (FE PROTEIN) (FRAGMENT).
GN NIFH.
OS unidentified nitrogen-fixing bacteria.
OC Bacteria.
OX NCBI_TaxID=34107;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohkuma M., Noda S., Kudo T.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB011937; BAA28471.1; -
DR HSSP; P00456; ICP2.
DR InterPro: IPR000392; -
DR Pfam: PF00142; fer1_nifh; 1.
DR PRINTS; PR00091; NITROGNASEII.
DR PROSITE; PS00746; NIFH_FRXC_1; 1.
DR PROSITE; PS00692; NIFH_FRXC_2; 1.
FT NON_TER 1
FT 142 142
SQ SEQUENCE 142 AA; 15173 MW; 8B68AC6B1B20C9A4 CRC64;

Query Match 100.0%; Score 26; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVDV 5
|||||
Db 106 KVDV 110

RESULT 12
O9ZVF3 PRELIMINARY; PRT; 151 AA.
AC O9ZVF3;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE PUTATIVE MAJOR LATEX PROTEIN.
GN F219.14.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
RA Shen M., Romling C.M., Fraser C.M., Somerville C.R., Venter J.C.;
RT "Arabidopsis thaliana chromosome II BAC F219 genomic sequence."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005560; AAC67328.1; -
DR Mendel; 33968; Arach;1544;33968.
SQ SEQUENCE 151 AA; 17513 MW; CDD237FA88EFAECB CRC64;

Query Match 100.0%; Score 26; DB 10; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVDV 5
|||||
Db 96 KVDV 100

RESULT 13
O9SU09 PRELIMINARY; PRT; 151 AA.
ID O9SU09
AC O9SU09;

DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE PUTATIVE MAJOR LATEX PROTEIN.
GN F9D16.150 OR ATAC23680.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Wedler H., Wambutt R., Hohensei J., Mewes H.W.,
RA Mayer K.F.X., Schueller C.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Wedler H., Wedler E., Wambutt R., Mewes H.W., Lemcke K.,
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035394; CAA23034.1; -
DR EMBL; AL161559; CAB79323.1; -
SQ SEQUENCE 151 AA; 17474 MW; D8726BA25EA1725A CRC64;

Query Match 100.0%; Score 26; DB 10; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVDV 5
|||||
Db 96 KVDV 100

RESULT 14
O82979 PRELIMINARY; PRT; 155 AA.
ID O82979
AC O82979;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE A2-5A ORF8.
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1409;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohdan K., Kuriki T.;
RT "Alkalophilic Bacillus DNA fragment involving MBP, CGTase, CDase
RT gene."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB015670; BAA31536.1; -
SQ SEQUENCE 155 AA; 17953 MW; F50EAD0C98D2D7E CRC64;

Query Match 100.0%; Score 26; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVDV 5
|||||
Db 75 KVDV 79

RESULT 15

Q39132
ID Q39132 PRELIMINARY; PRT: 155 AA.
AC Q39132;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)
DE MAJOR LATEX PROTEIN TYPE1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-COL 0;
RA Grelliet F., Cooke R., Laudie M., Raynal M., Delseny M.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; X91960; CAA63026.1; -
DR Mendel; 7159; Arath;1544;7159.
SQ SEQUENCE 155 AA; 17892 MW; EA4D9858B70AF205 CRC64;

Query Match 100.0%; Score 26; DB 10; Length 155;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KYYDV 5
|1111|
Db 96 KYYDV 100

Search completed: August 9, 2001, 20:36:16
Job time: 715 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 9, 2001, 20:24:13 ; Search time 79.24 Seconds
(without alignments)
3.060 Million cell updates/sec

Title: US-09-367-013B-2_COPY_50_53
Page: 37

Sequence:

1 НРGG

Scoring table:	BLOSUM62	Canopy 10 0	Canopy 0 5
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Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Database :

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3:	/SIDS8/gcgcata/gemseq/gemseqp/AA1982..DAT.*
4:	/SIDS8/gcgcata/gemseq/gemseqp/AA1983..DAT.*
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21:	/SIDS8/gcgcata/gemseq/gemseqp/AA2000..DAT.*
22:	/SIDS8/gcgcata/gemseq/gemseqp/AA2001..DAT.*

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	27	100.0	5	12	AAK12709	Pentapeptide paral
2	27	100.0	5	13	AAK51573	Mimotope peptide #
3	27	100.0	5	16	AAK69941	Pentameric mimotop
4	27	100.0	5	17	AAK98687	Peptide 67 from 88
5	27	100.0	14	20	AAV08373	Cysteine noose lib
6	27	100.0	15	21	AAK11403	C. maltosa cytochro
7	27	100.0	22	16	AAK65097	Random biotinylati
8	27	100.0	23	19	AAW46700	Biotinylation pep
9	27	100.0	23	20	AAV29303	Biotinylation pep
10	27	100.0	25	20	AAV43562	Human prostate can
11	27	100.0	38	19	AAW42450	C. neoformans Mfal

12	27	100.0	38	22	AAB31646	Amino acid sequenc
13	27	100.0	41	21	AAB12188	Gastro-intestinal
14	27	100.0	42	20	AAV25795	Human secreted pro
15	27	100.0	42	21	AAAG27100	Zea mays protein f
16	27	100.0	43	21	AAAG35334	Zea mays protein f
17	27	100.0	48	21	AAAB3231	CYB5RP fatty acid
18	27	100.0	48	21	AAAB3232	Cytochrome b5 pept
19	27	100.0	49	22	AAAB31651	Amino acid sequenc
20	27	100.0	51	20	AAV48336	Human prostrate can
21	27	100.0	53	21	AAAB3235	CYB5RP fatty acid
22	27	100.0	53	21	AAAB3236	Sunflower hypochet
23	27	100.0	53	21	AAAB3241	CYB5RP fatty acid
24	27	100.0	53	21	AAAB3242	Delta 6 desaturase
25	27	100.0	57	21	AAAG27909	Arabidopsis thaliaa
26	27	100.0	59	21	AAAG19063	Zea mays protein f
27	27	100.0	67	19	AAAB3944	Human secreted pro
28	27	100.0	69	21	AAAB3230	Murine CYB5RP fatt
29	27	100.0	69	22	AAAB64663	Human secreted pro
30	27	100.0	70	21	AAAY75953	Murine skin cell p
31	27	100.0	70	22	AAAB55882	Skin cell protein,
32	27	100.0	71	21	AAAG16088	Arabidopsis thaliaa
33	27	100.0	74	21	AAAG27110	Zea mays protein f
34	27	100.0	78	20	AAAY48225	Human prostrate can
35	27	100.0	78	21	AAAG27059	Zea mays protein f
36	27	100.0	78	21	AAAY69169	A patial human N-a-
37	27	100.0	79	21	AAAG35333	Zea mays protein f
38	27	100.0	80	21	AAAG32672	Zea mays protein f
39	27	100.0	85	21	AAAY58763	Rice DAHP syncheta
40	27	100.0	88	21	AAAG18777	Zea mays protein f
41	27	100.0	95	21	AAAG19062	Zea mays protein f
42	27	100.0	96	21	AAAG27908	Arabidopsis thaliaa
43	27	100.0	97	20	AAAY13084	Human secreted pro
44	27	100.0	97	21	AAAB40091	Anti-hlil2 antibod
45	27	100.0	98	21	AAAG07990	Arabidopsis thaliaa

ALIGNMENTS

RESULT 1

ID	AA	standard; 5 AA.
1	AA12709	standard; 5 AA.

AC AAR12709;

DT 31-JUL-1991 (first entry)

DE Pentapeptide paralogue for use as chromatographic affinity ligand

KW HPLC.

OS Synthetic

PN W09106356-A.

PD 16-MAY-1991
VY

PF 31-OCT-1990; 90WO-EP063333.

PR 31-OCT-1989; 8905-0429/21.
XY

PA (TERR-) TERRAPIN TEECHN INC.
XX

[illegible][illegible]

PT Identifying paralog with specific affinity for analyte - using
PT candidate paralogs with systematically varied values of at least
PT 2 parameters.

PS Claim 41; Fig 8; 95pp; English.

CC Peptide is one of a panel, each of which have systemically varied
 CC values of at least two parameters. A test protein is matched against
 CC the panel, and the paralogues with highest binding affinity are
 CC selected. Selected paralogues are bound to a matrix which is
 CC incorporated into the HPLC gel and used as affinity ligands.
 CC Technique is useful in chromatographic separation, purification
 CC and binding assay.

XX
 SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 12; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPGG 4
 ||||
 Db 2 hp9g 5

RESULT 2

AA851573
 ID AAR51573 standard; peptide; 5 AA.

XX AAR51573;

DT 19-OCT-1994 (first entry)

XX Mimotope peptide #67 from panel of maximally diverse mimotopes.

XX mimotope panel; rational drug design; candidate drug;
 KW screening assay; hydrophobicity; antibody repertoire.

XX Synthetic.

OS
 FH Key Location/Qualifiers

FT Modified-site 1 /note="acetylated"

XX US5300425-A.

XX 05-APR-1994.

PF 13-OCT-1987; 87US-0108130.

XX 13-OCT-1987; 87US-0108130.

PR 11-OCT-1988; 88US-0255906.

PR 06-DEC-1989; 89US-0447009.

XX (TERR-) TERRAPIN TECHNOLOGIES INC.

XX Kauvar LM;

XX WPI; 1994-109390/13.

PT Screening of candidate drugs for binding to receptor - by
 PT comparing inverse image antibody profile of drug with
 PT mimotype binding profile of receptor

XX Example 3; Fig 3; 29pp; English.

CC A panel of 88 pentapeptides was designed on the basis of decreasing
 CC hydrophobicity and periodic variation of hydrophobic moment. The
 CC peptides were labelled with iodine-125 and tested with individual
 CC members of a basal antibody repertoire. (Spleen cells were
 CC harvested from mice and used to provide a panel of
 CC antibody-secreting hybridoma cells as a subset of the complete
 CC B-cell repertoire). Nearly uniform binding to all antibody members
 CC of the repertoire was observed. The test was than repeated with the
 CC addition of a defined amount of analyte to the mixture. A small
 CC number of wells showed greatly decreased labelling and these
 CC antibodies represented the successful result of an initial screen
 CC for those which preferentially bind analyte.

XX
 SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 15; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPGG 4
 ||||
 Db 2 hp9g 5

RESULT 3

AA869941
 ID AAR69941 standard; peptide; 5 AA.

XX AAR69941;

DT 18-OCT-1995 (first entry)

XX Pentameric mimotope 67 used to obtain highly specific antibodies.

XX mimotope; antibody; production; high specificity; detection;
 KW immunoassay; high performance liquid chromatography.

XX Synthetic.

OS
 FH Key Location/Qualifiers

FT Modified-site 1 /note="Acetyl-Asn"

XX US5384263-A.

XX 24-JAN-1995.

PF 13-OCT-1987; 87US-0108130.

XX 13-OCT-1987; 88US-0255906.

PR 13-OCT-1987; 87US-0108130.

PR 04-JUN-1993; 93US-0072190.

XX (TERR-) TERRAPIN TECHNOLOGIES INC.

XX Kauvar LM;

XX WPI; 1995-105497/14.

PT Producing antibodies with high specificity and affinity for an
 PT analyte - by immunisation with selected mimotope, also analyte
 PT detection kits, useful for immunoassay of materials usually
 PT analysed by HPLC

XX Example 3; Fig 3; 25pp; English.

CC AAR69875-969 are pentameric mimotopes designed on the basis of
 CC decreasing hydrophobicity and periodic variation of hydrophobic
 CC moment. All the pentapeptides are acetylated at the N-terminus except
 CC E12 (for FITC) (sic). E12 is not identified in the specification.
 CC The mimotopes are used in the method of the invention to obtain
 CC antibodies specifically and strongly reactive with a desired
 CC analyte. The mimotope is obtained by reacting a panel of starting
 CC antibodies (Abs) representative of the resting B cell repertoire of a
 CC mammal with an analyte (so as to identify analyte-reacting Abs) and
 CC then reacting each of a panel of candidate mimotopes representative
 CC of a random set of 3D contours with the analyte-reacting Abs. A
 CC subject is immunised with one or more mimotopes identified and the
 CC product Abs are recovered from the serum of the subject.

XX Sequence 5 AA;

Query Match 100.0%; Score 27; DB 16; Length 5;

Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPGC 4
||||
Db 2 hp9g 5

RESULT 4

AAR98687
ID AAR98687 standard; peptide; 5 AA.

AC AAR98687;

DT 11-MAR-1997 (first entry)

DE Peptide 67 from 88 member diverse mimotope panel.

Panel: mimotope; decreasing hydrophobicity; periodic variation;
hydrophobic moment; antibody; repertoire; identification; drug;
candidate; receptor; binding; ligand; rational; design; selection;
treatment; tumour; production; immunological reagent; analyte;
detection; trace contaminant; mimotope.

OS Synthetic.

Key Location/Qualifiers
Modified-site 1 /note="acylated"

PN US5541070-A.

PD 30-JUL-1996.

PE 13-OCT-1987; 87US-0108130.

PR 06-DEC-1989; 89US-0447009.

PR 13-OCT-1987; 87US-0108130.

PR 11-OCT-1988; 88US-0255906.

PR 08-SEP-1993; 93US-0118133.

PA (KAUV/) KAUVAR L M.

PI KAUVAR LM;

PS WPL; 1996-361955/36.

PT Identifying candidate drugs that bind a specific receptor by
competitive reaction with panel of mimotope(s) - useful in rational
drug design

XX Example 3; Fig 3; 27pp; English.

XX The present peptide is a member of a panel of 88 pentapeptide

XX mimotopes designed on the basis of decreasing hydrophobicity, and

XX periodic variation of hydrophobic moment. The panel was synthesised

XX using the method of Geysen, H. M., et al, Proc. Natl. Acad. Sci.

XX USA (1988), which uses lots of 96 pins; the remaining 8

XX polyethylene pins being controls. The mimotopes were then mixed,

XX 155-1 labelled and tested with individual members of a basal

XX antibody (Ab) repertoire. Nearly uniform binding to all members was

XX found. The test was then repeated with the addition of a defined

XX ant. of analyte. A small number showed greatly increased labelling,
XX these Ab representing the successful result of an initial screen
XX for those that pref. bind analyte.

XX The above is an example of a claimed method for identifying members
XX of a panel of candidate drugs, that bind to a receptor having a
XX known ligand. It is useful in rational drug design, e.g. selection
XX of monoclonal Ab for treating individual tumours, and for the prodn.
XX of immunological reagents for any analyte, including those not
XX normally detectable by immunoassay, e.g trace contaminants in soil,
XX air or water.

SQ Sequence 5 AA:

Query Match 100.0%; Score 27; DB 17; Length 5;

Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPGC 4
||||
Db 2 hp9g 5

RESULT 5

AAV08373
ID AAV08373 standard; Protein; 14 AA.

AC AAV08373;

DT 28-JUL-1999 (first entry)

DE Cysteine noose library SCFV VH CDR3 clone M11 peptide.

Cysteine noose; antibody variable domain; CDR; cytokine; agonist;
complementarity determining region; antagonist; mimetic; antigen;
MIP-1 alpha receptor; treatment; HIV infection; CDR3; anti-HIV.

OS Synthetic.

PN W09923222-A1.

PD 14-MAY-1999.

PE 30-OCT-1998; 98WO-GB03255.

PR 31-OCT-1997; 97GB-0023062.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Osbourne JK;

PS WPL; 1999-313343/26.

PT Cysteine noose antibody libraries and their production

XX Example 5; Page 41; 64pp; English.

XX This invention describes the construction of libraries of antibody

XX variable domains containing modified complementarity determining regions

XX (CDRs) carrying a cysteine noose and which have cytokine agonist and

XX antagonist mechanisms of action. The method of the invention can be used

XX to obtain peptide ligand mimetics capable of binding a target antigen.

XX The binding members may also be used to provide agonists or antagonists

XX of targets such as cytokines. In particular specific binding members for

XX MIP-1 alpha receptors are useful for treatment of HIV infection and for

XX peptide ligand mimetics from CDR3 cysteine noose libraries provide a

XX means to select a different and potentially more effective population of

XX peptide ligands than direct display of similar cysteine noose ligands on

XX anti-HIV activity. AAV08352-Y08378 and AAV08362-Y08398 are peptides used

XX in the method of the invention.

SQ Sequence 14 AA:

Query Match 100.0%; Score 27; DB 20; Length 14;

Best Local Similarity 100.0%; Pred. No. 49;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPGC 4
||||
Db 11 hp9g 14

```
RESULT 6
AAB11403
ID AAB11403 standard; peptide; 15 AA.
XX
AC AAB11403;
XX
DT 22-FEB-2001 (first entry)
XX
DE C. maltosa cytochrome b5 peptide fragment 753.
XX
KM Cytochrome b5; alkane metabolism; oxidation; long-chain alkyl compound;
KW long-chain dicarboxylic acid.
XX
OS Candida maltosa.
XX
PN WO200065061-A2.
XX
PD 02-NOV-2000.
XX
PF 18-APR-2000; 2000WO-DE01246.
XX
PR 24-APR-1999; 99DE-1018763.
XX
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI Schunck W, Chernogolov A;
XX
DR WPI: 2000-679674/66.
XX
PT Nucleic acid sequences from alkane metabolizing Candida yeast, encoding
PR cytochrome b5 and used for the oxidation of long chain alkyl compounds
XX and for the production of long chain dicarboxylic acids -
XX
PS Example 1.2; Page 6; 27pp; German.
XX
CC This invention describes novel nucleic acid sequences from alkane
CC metabolizing Candida yeasts, encoding cytochrome b5-polypeptide, its
CC fragments, variants and mutations. The nucleic acids and polypeptides
CC are used for the oxidation of long-chain alkyl compounds with at least
CC 10C, and for the production of long-chain dicarboxylic acids by oxidizing
CC n-alkanes and fatty acids with at least 10C.
XX
SQ Sequence 15 AA:

Query Match 100.0%; Score 27; DB 21; Length 15;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
   ||||
Db 11 hp9g 14

RESULT 7
AAR65097
ID AAR65097 standard; peptide; 22 AA.
XX
AC AAR65097;
XX
DT 25-OCT-1995 (first entry)
XX
DE Random biotinylation peptide 62.
XX
KM biotinylation; peptide; recombinant; fusion protein; small;
KW specific; defined; purification; Birt; enzyme; biotin.
XX
OS Synthetic.
XX
PA Key
XX Key Location/Qualifiers
XX Misc-difference 6 /note= "encoded by a supE suppressed amber codon"
XX
```

```
FT Modified-site 13
FT /note= "Biotin-Lys"
XX
XX
PN WO9504069-A.
XX
PD 09-FEB-1995.
XX
PF 28-JUL-1994; 94WO-US08528.
XX
PR 30-JUL-1993; 93US-0099991.
XX
PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX
PI Schatz PJ;
XX
DR WPI: 1995-090609/12.
XX
PT Production of biotinylated proteins by expression of a
PR recombinant DNA vector - which encodes a fusion protein
XX comprising a protein and a biotinylated peptide.
XX
PS Claim 10; Page 137; 146pp; English.
XX
XX
CC AAR65091-106 are biotinylated peptides that were designed to fit the
CC consensus sequence of the invention and a random peptide (AAR65090).
CC The library was made so that the biotinylation peptides would be
CC expressed in a fusion protein at the N-terminus of cytoplasmic MBP.
CC A host cell, eg. E. coli is transformed with the fusion gene and is
CC cultured in the presence of biotin and a biotinylation enzyme, eg. Birt.
CC This library was used to explore the general utility of biotinylated
CC peptides and to expand their possible uses.
XX
SQ Sequence 22 AA:

Query Match 100.0%; Score 27; DB 16; Length 22;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
   ||||
Db 18 hp9g 21

RESULT 8
AAW46700
ID AAW46700 standard; peptide; 23 AA.
XX
AC AAW46700;
XX
DT 28-MAY-1998 (first entry)
XX
DE Biotinylation peptide expressed at the N-terminus of MBP.
XX
KM Biotinylation peptide; biotinylation enzyme; biotin-protein ligase;
KW Birt; biotin ligase; biotin; purification; immobilisation; labelling;
KW detection; protein; melrose binding protein; MBP.
XX
OS Synthetic.
XX
PN US5723584-A.
XX
PD 03-MAR-1998.
XX
PF 03-FEB-1995; 95US-0383753.
XX
PR 30-JUL-1993; 93US-0099991.
XX
PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX
PI Schatz PJ;
XX
DR WPI: 1998-178542/16.
```

XX peptide(s) that can be biotinylated by biotin ligase - and fusion
PT proteins containing them
XX
PS Claim 3: Column 68: 33pp: English.
XX
CC Peptides AAM46694-709 are non-naturally occurring biotinylation
CC peptides, derived from a library constructed to express peptides of the
CC sequence AAM46693. The library was made so that the biotinylation
CC peptides are expressed in a fusion protein at the N-terminus of
CC cytoplasmic melrose binding protein (MBP). The ability to express
CC functional biotinylation sequences free at either end of a protein
CC indicates that there is no requirement that either end of the peptide be
CC free in order to interact with the biotin holoenzyme synthetase. The
CC peptides can be biotinylated in vitro or in vivo, especially with Bira
CC biotin ligase, and used for the purification, immobilisation, labelling
CC or detection of proteins.
XX
SQ Sequence 23 AA:

Query Match 100.0%; Score 27; DB 19; Length 23;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
|
|
|
|
DB 19 hpqg 22

RESULT 9
ID AAY29303 standard; peptide; 23 AA.
XX
AC AAY29303;
XX
DT 28-SEP-1999 (first entry)
XX
DE Biotinylation peptide SEQ ID NO:80.
XX
KW Biotinylation enzyme; biotin-protein ligase; Bira; labelling;
KM biotin carboxyl carrier protein; BCCP; Escherichia coli;
XX fusion protein; identification; purification; diagnosis; research.
XX
OS Escherichia coli.
XX Synthetic.
XX
PN US932433-A.
XX
PD 03-AUG-1999.
XX
PF 28-OCT-1997; 97US-0959512.
XX
PR 03-FEB-1995; 95US-0383753.
PR 30-JUL-1993; 93US-0099991.
PR 28-OCT-1997; 97US-0959512.
XX
PA (AFET-) AFFYMAX TECHNOLOGIES NV.
XX
PI Schatz PJ;
XX
DR WPI; 1999-457113/38.
XX
PT Identification and biotinylation of proteins synthesized by
XX recombinant DNA techniques in vivo
XX
PS Claim 6: Column 68: 35pp: English.
XX
CC The present invention describes a method for the identification and
CC biotinylation of proteins synthesized by recombinant DNA techniques
CC in vivo with a biotinylation peptide of less than 50 amino acids. The
CC method comprises: (a) on the surface of a substrate, providing a fusion
CC protein comprising a recombinant protein and a peptide defined by the

CC sequence given in AAY24492, where the peptide is capable of being
CC biotinylated by a biotin ligase at the lysine residue adjacent to
CC position 8 and is 13-50 aa in length; (b) in a predefined region of the
CC surface of the substrate, contacting the fusion protein with an enzyme;
CC and (c) determining whether the fusion protein has been biotinylated.
CC The method allows the identification and purification of biotinylated
CC enzymes e.g. Bira. The method is also useful in research and diagnostic
CC applications. The method uses small but specific peptides, allowing the
CC labelling of a protein at a defined site, this provides improved
CC immobilization and avoids the use of antibodies. AAY24493 to AAY24548,
CC and AAY29299 to AAY29312 represent specifically claimed examples of
CC biotinylation peptides for use in the method of the invention.
XX
SQ Sequence 23 AA:

Query Match 100.0%; Score 27; DB 20; Length 23;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
|
|
|
|
DB 19 hpqg 22

RESULT 10
ID AAY48362 standard; Protein; 25 AA.
XX
AC AAY48362;
XX
DT 08-DEC-1999 (first entry)
XX
DE Human prostate cancer-associated protein 59.
XX
KW Expressed sequence tag; EST; prostate; tumor; treatment; gene therapy;
KM cancer; tissue specificity; human.
XX
OS Homo sapiens.
XX
PN DE19811194-A1.
XX
PD 16-SEP-1999.
XX
PF 10-MAR-1998; 98DE-1011194.
XX
PR 10-MAR-1998; 98DE-1011194.
XX
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
PI Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
XX
DR WPI; 1999-519629/44.
XX
DR N-PSDB; AA233504.
XX
PT New nucleic acid expressed at high level in normal prostatic tissue and
PT encoded polypeptides, used to treat cancer and screen for therapeutic
XX agents -
XX
PS Claim 22: 146; 194pp; German.
XX
CC This invention describes novel nucleic acid sequences (A) that are
CC expressed at high level in normal prostatic tissue. Polypeptides (I)
CC encoded by (A) are used: (a) for identifying agents for treatment of
CC prostatic cancer and (b) for therapy of prostate cancer, optionally
CC where expressed by gene therapy methods. (A) is also used to isolate
CC full-length genes (for gene therapy) and for recombinant production of
CC (I), which can be used to raise specific antibodies. (A) are identified
CC by assembly of ESTs (expressed sequence tags) before these are analyzed
CC for expression pattern (tissue specificity). This approach eliminates
CC many of the false results, as regards tissue specificity, associated
CC with known methods that use single (usually short) ESTs. AAY48304-Y48456
CC represent peptides encoded by the expressed sequence tags described in

XX AAB12198;
 AC 10-NOV-2000 (first entry)
 DT XX
 DE Gastro-Intestinal tract transport receptor targeting agent ZELan024.
 KW Gastro-Intestinal tract; GIT; transport receptor; drug transport;
 KM targeting agent; antibody generation.
 OS Unidentified.
 XX WO200031546-A1.
 PN 02-JUN-2000.
 PD 19-NOV-1999; 99WO-IE00116.
 PE 19-NOV-1998; 98US-0109036.
 PR (ELAN-) ELAN CORP PLC.
 PA O'Mahony DJ, Seveso M;
 PI WPI; 2000-451689/39.
 DR Antibody specific to a domain of a gastrointestinal (GIT) targeting
 PT agent such as ZELan033, ZELan088 and ZELan053, useful for detecting,
 PT quantitating and locating GIT targeting agents -
 XX Disclosure; Fig 5; 24pp; English.
 PS
 XX The present sequence is gastro-intestinal tract (GIT) transport receptor
 CC targeting agent, ZELan024. This peptide is capable of facilitating
 CC transport of an active agent e.g. a drug through gastro-intestinal
 CC tissue. The present sequence may be used as an immunogen, for the
 CC generation of antibodies which specifically bind to the present sequence.
 CC The GIT transport receptor targeting agent antibodies are useful for
 CC detecting, quantitating and locating the GIT transport receptor targeting
 CC agents.
 XX
 SO Sequence 41 AA:
 Query Match 100.0%; Score 27; DB 21; Length 41;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HPGC 4
 IIII
 Db 38 hpgg 41
 RESULT 14
 AAY25795
 ID AAY25795 standard; Protein: 42 AA.
 XX
 AC AAY25795;
 DT 04-OCT-1999 (first entry)
 DE Human secreted protein fragment encoded from gene 12.
 DE
 XX Secreted protein: human; treatment; diagnosis; therapy; cancer; tumour;
 KM neurodegenerative disorder; developmental abnormality; blood disorder;
 KM fetal deficiency; blood disorder; leukemia; immune system; inflammation;
 KM autoimmune disease; hepatic disease; renal disease; allergy; restenosis;
 KM ischaemic shock; Alzheimer's disease; cognitive disorder; schizophrenia;
 KM cardiovascular disorder; wound healing; stroke; arthritis; obesity;
 KM asthma; sepsis; acne; psoriasis; transplant rejection; infection; AIDS;
 KM metabolic disorder.
 XX
 OS Homo sapiens.

XX WO9938881-A1.
 PN 05-AUG-1999.
 PD XX
 DE 27-JAN-1999; 99WO-US01621.
 KW 30-JAN-1998; 98US-0073170.
 PR 30-JAN-1998; 98US-0073159.
 PR 30-JAN-1998; 98US-0073160.
 PR 30-JAN-1998; 98US-0073161.
 PR 30-JAN-1998; 98US-0073162.
 PR 30-JAN-1998; 98US-0073164.
 PR 30-JAN-1998; 98US-0073165.
 PR 30-JAN-1998; 98US-0073167.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Carter KC, Endress GA, Feng P, Ferrle AM, Florence C;
 PI Florence KA, Janat F, Nl J, Rosen CA, Ruben SM;
 PI Soppet DR, Young P, Yu G;
 XX
 DR WPI: 1999-469315/39.
 DR N-PSDB: AA200421.
 XX
 PT New isolated human genes and the secreted polypeptides they encode
 PT useful in, e.g. treatment of Alzheimer's
 XX
 PS Disclosure; Page 348-349; 393pp; English.
 XX
 XX This invention describes novel human genes (see AA200410-200477) and the
 CC secreted proteins (see AAY25711-Y25778) and fragments (see
 CC AA25779-Y25907) they encode. The polynucleotides and their corresponding
 CC secreted polypeptides are useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. Also pathological
 CC conditions can be diagnosed by determining the amount of the new
 CC polypeptides in a sample or by determining the presence of mutations in
 CC the new polynucleotides. Specific uses are described for each of the 67
 CC polynucleotides of the invention, based on which tissues they are most
 CC highly expressed in, and include developing products for the diagnosis
 CC or treatment of cancer, tumours, neurodegenerative disorders,
 CC developmental abnormalities and fetal deficiencies, blood disorders,
 CC leukemias, diseases of the immune system, autoimmune diseases, hepatic
 CC and renal disease, inflammation, allergies, ischaemic shock, Alzheimer's
 CC and cognitive disorders, schizophrenia, restenosis, cardiovascular
 CC disorders, wound healing, stroke, arthritis, obesity, asthma, sepsis,
 CC acne, psoriasis, transplant rejection, metabolic disorders, infections
 CC and AIDS. The polypeptides are also useful for identifying their binding
 CC partners.
 XX
 SO Sequence 42 AA:
 Query Match 100.0%; Score 27; DB 20; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HPGC 4
 IIII
 Db 25 hpgg 28
 RESULT 15
 AAG27100
 ID AAG27100 standard; Protein: 42 AA.
 XX
 AC AAG27100;
 DT 17-OCT-2000 (first entry)
 DE Zea mays protein fragment SEQ ID NO: 31806.
 DE
 XX Protein identification; signal transduction pathway; metabolic pathway;
 KW

KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence; corn.
OS Zea mays subsp. mays.
XX EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132487.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 18-MAY-1999; 99US-0134370.
PR 19-MAY-1999; 99US-0134768.
PR 20-MAY-1999; 99US-0134941.
PR 21-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
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PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
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PR 18-JUN-1999; 99US-0139460.
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PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
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PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
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PR 30-JUN-1999; 99US-0141287.
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PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
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PR 06-AUG-1999; 99US-0147416.
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PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.

PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0156559.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
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 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
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 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 100.0%; Score 27; DB 21; Length 42;

Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
 Db 4 hpgg 7

Search completed: August 9, 2001, 20:24:14
 Job time: 248 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 9, 2001, 20:25:05 ; Search time 45.84 seconds
(without alignments)
1.797 Million cell updates/sec

Title: US-09-367-013b-2_COPY_50_53
Perfect score: 27
Sequence: 1 HPGG 4

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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6: /cgn2_6/prodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	27	100.0	5	6	5217869-67	Patent No. 5217869
2	27	100.0	15	2	US-08-811-028-52	Sequence 52, Appl
3	27	100.0	23	1	US-08-383-753-80	Sequence 80, Appl
4	27	100.0	23	2	US-08-586-772-80	Sequence 80, Appl
5	27	100.0	23	2	US-08-959-512-80	Sequence 80, Appl
6	27	100.0	40	2	US-08-751-767A-63	Sequence 63, Appl
7	27	100.0	70	4	US-09-188-930-131	Sequence 131, App
8	27	100.0	91	3	US-08-851-843A-220	Sequence 220, App
9	27	100.0	91	4	US-08-974-549A-339	Sequence 339, App
10	27	100.0	97	4	US-08-905-223-368	Sequence 368, App
11	27	100.0	104	2	US-08-801-972-5	Sequence 5, Appl
12	27	100.0	104	3	US-09-178-881-5	Sequence 5, Appl
13	27	100.0	134	2	US-08-801-972-4	Sequence 4, Appl
14	27	100.0	134	3	US-09-178-881-4	Sequence 4, Appl
15	27	100.0	144	3	US-09-041-517-1	Sequence 1, Appl
16	27	100.0	142	2	US-08-801-972-3	Sequence 3, Appl
17	27	100.0	142	3	US-09-178-881-3	Sequence 3, Appl
18	27	100.0	155	2	US-08-801-972-1	Sequence 1, Appl
19	27	100.0	155	3	US-09-178-881-1	Sequence 1, Appl
20	27	100.0	297	3	US-09-173-581-1	Sequence 1, Appl
21	27	100.0	353	1	US-08-118-270-45	Sequence 45, Appl
22	27	100.0	353	5	PCT-US93-08528-45	Sequence 45, Appl
23	27	100.0	426	1	US-07-918-023-2	Sequence 2, Appl
24	27	100.0	431	4	US-09-416-050A-8	Sequence 8, Appl
25	27	100.0	431	4	US-09-664-800-8	Sequence 8, Appl
26	27	100.0	431	4	US-09-665-309-8	Sequence 8, Appl
27	27	100.0	431	4	US-09-661-569-8	Sequence 8, Appl

28	27	100.0	440	1	US-07-930-686-12	Sequence 12, Appl
29	27	100.0	440	2	US-08-460-998-12	Sequence 12, Appl
30	27	100.0	446	2	US-08-833-610-2	Sequence 2, Appl
31	27	100.0	446	2	US-08-833-610-5	Sequence 5, Appl
32	27	100.0	446	3	US-08-834-033A-5	Sequence 5, Appl
33	27	100.0	446	3	US-08-834-033A-15	Sequence 15, Appl
34	27	100.0	448	1	US-08-366-779-5	Sequence 5, Appl
35	27	100.0	448	1	US-08-789-936-5	Sequence 5, Appl
36	27	100.0	455	1	US-08-035-928-2	Sequence 2, Appl
37	27	100.0	457	2	US-08-834-655-2	Sequence 2, Appl
38	27	100.0	457	2	US-08-833-610-4	Sequence 4, Appl
39	27	100.0	457	3	US-08-834-033A-2	Sequence 2, Appl
40	27	100.0	457	3	US-08-834-033A-14	Sequence 14, Appl
41	27	100.0	457	4	US-09-363-574-2	Sequence 2, Appl
42	27	100.0	508	2	US-08-861-464-10	Sequence 10, Appl
43	27	100.0	508	2	US-08-396-001-10	Sequence 10, Appl
44	27	100.0	508	4	US-09-323-433A-10	Sequence 10, Appl
45	27	100.0	510	1	US-08-742-273-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
5217869-67
Patent No. 5217869
APPLICANT: KAUVAR, LAWRENCE M.
TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC REAGENTS
NUMBER OF SEQUENCES: 121
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/255,906
FILING DATE: 11-OCT-1988
SEQ ID NO:67:
LENGTH: 5
5217869-67

Query Match 100.0%; Score 27; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 HPGG 4
Db 2 HPGG 5

RESULT 2
US-08-811-028-52
Sequence 52, Application US/08811028C
Patent No. 5891671
GENERAL INFORMATION:
APPLICANT: SUZUKI, YUJI
APPLICANT: MAGOTA, KOJI
TITLE OF INVENTION: METHOD FOR CLEAVING CHIMERIC ENZYME USING PROCESSING
TITLE OF INVENTION: ENZYME
FILE REFERENCE: 001560-294
CURRENT APPLICATION NUMBER: US/08/811,028C
CURRENT FILING DATE: 1987-03-04
EARLIER APPLICATION NUMBER: JP 8-70906
EARLIER FILING DATE: 1996-03-04
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 52
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: modified
OTHER INFORMATION: Kex2-660 recognition site; x is gly, ala, val,
OTHER INFORMATION: leu, ile, ser, thr, asp, glu, asn, gln, lys, arg,
OTHER INFORMATION: phe, tyr, trp, his, or pro

US-08-811-028-52

Query Match 100.0%; Score 27; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
1111
DB 5 HPGG 8

RESULT 3

US-08-383-753-80
; Sequence 80, Application US/08383753
; Patent No. 5723584
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; TITLE OF INVENTION: Biotinylation of Proteins
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,753
; FILING DATE: 03-FEB-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/099,991
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 1038.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-383-753-80

Query Match 100.0%; Score 27; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
1111
DB 19 HPGG 22

RESULT 4

US-08-586-772-80
; Sequence 80, Application US/08586772
; Patent No. 5874239
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; TITLE OF INVENTION: Biotinylation of Proteins
; NUMBER OF SEQUENCES: 102

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,772
; FILING DATE: 03-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/099,991
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 1038.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-586-772-80

Query Match 100.0%; Score 27; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
1111
DB 19 HPGG 22

RESULT 5
US-08-959-512-80
; Sequence 80, Application US/08959512
; Patent No. 5932433
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; TITLE OF INVENTION: Biotinylation of Proteins
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/959,512
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/383,753
; FILING DATE: 03-FEB-1995
; APPLICATION NUMBER: US 08/099,991

FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1038.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-959-512-80

Query Match 100.0%; Score 27; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGC 4
1111
DB 19 HPGC 22

RESULT 6
US-08-751-767A-63
Sequence 63, Application US/08751767A
Patent No. 5994104
GENERAL INFORMATION:
APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 117-221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164091
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-751-767A-63

Query Match 100.0%; Score 27; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGC 4
1111
DB 27 HPGC 30

RESULT 7
US-09-188-930-131
Sequence 131, Application US/09188930A
Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
FILE REFERENCE: 11000.101c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 131
LENGTH: 70
TYPE: PRT
ORGANISM: mouse
US-09-188-930-131

Query Match 100.0%; Score 27; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGC 4
1111
DB 51 HPGC 54

RESULT 8
US-08-851-843A-220
Sequence 220, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-0029300S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 220:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-851-843A-220

Query Match 100.0%; Score 27; DB 3; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
1111
DB 75 HPGG 78

RESULT 9
US-08-974-549A-339
Sequence 339, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morlin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-0026100S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 339:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-339

Query Match 100.0%; Score 27; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
1111
DB 75 HPGG 78

RESULT 10
US-08-905-223-368
Sequence 368, Application US/08905223
Patent No. 6222029
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Ducloux, Aymeric
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:

NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 368:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
TISSUE TYPE: Brain
FEATURE:
NAME/KEY: sig-peptide
LOCATION: 21...1
IDENTIFICATION METHOD: Von Heijne matrix
OTHER INFORMATION: score 4.1
OTHER INFORMATION: seq GLWAHSWTCSCSA/AX
US-08-905-223-368

Query Match 100.0%; Score 27; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPGG 4
Db 27 HPGG 30

RESULT 11

US-08-801-972-5
Sequence 5, Application US/08801972
Patent No. 5831018
GENERAL INFORMATION:
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: A NOVEL HUMAN CYTOCHROME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Incycle Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,972
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0216 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-4166
TELEFAX: 415-845-0555
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 1217655
US-08-801-972-5

Query Match 100.0%; Score 27; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPGG 4
Db 13 HPGG 16

RESULT 12

US-09-178-881-5
Sequence 5, Application US/09178881
Patent No. 6083704
GENERAL INFORMATION:
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: A NOVEL HUMAN CYTOCHROME B5
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Incycle Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/178,881
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/801,972
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0216 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-4166
TELEFAX: 415-845-0555
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 1217655
US-09-178-881-5

Query Match 100.0%; Score 27; DB 3; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPGG 4
Db 13 HPGG 16

RESULT 13

US-08-801-972-4
Sequence 4, Application US/08801972
Patent No. 5831018

GENERAL INFORMATION:
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOVEL HUMAN CYTOCHROME
NUMBER OF INVENTION: B5
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,972
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0216 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 476415
US-08-801-972-4

Query Match 100.0%, Score 27, DB 2, Length 134;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
1111
DB 44 HPGG 47

RESULT 14
US-09-178-881-4
Sequence 4, Application US/09178881
GENERAL INFORMATION:
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOVEL HUMAN CYTOCHROME B5
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/178,881

FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/801,972
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0216 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 476415
US-09-178-881-4

Query Match 100.0%, Score 27, DB 3, Length 134;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
1111
DB 44 HPGG 47

RESULT 15
US-09-041-517-1
Sequence 1, Application US/09041517
Patent No. 6107035
GENERAL INFORMATION:
APPLICANT: Squires, E. James
APPLICANT: Davis, Shawn
APPLICANT: Stegiles, Alan W.
APPLICANT: Vandermark, Petra
TITLE OF INVENTION: Method of Determining Predisposition to
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bereskin & Parr
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,517
FILING DATE: 13-MAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Michelle
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 6580-120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

; MOLECULE TYPE: peptide
 ; ORIGINAL SOURCE:
 ; ORGANISM: Porcine Cytochrome b5
 US-09-041-517-1

Query Match 100.0%; Score 27; DB 3; Length 134;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HPGG 4
 ||||
 Db 44 HPGG 47

Search completed: August 9, 2001, 20:25:06
 Job time: 205 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 9, 2001, 20:26:03 : Search time 50.69 seconds
(without alignments)
6.011 Million cell updates/sec

Title: US-09-367-013b-2_COPY_50_53

Perfect score: 27

Sequence: 1 HPGG 4

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	16	2 I51879	cystathionine beta
2	27	100.0	38	2 A48158	pheromone precursor
3	27	100.0	51	2 PQ0816	probable cytochrom
4	27	100.0	64	2 T05913	hypothetical prote
5	27	100.0	74	2 A41085	nitrate reductase
6	27	100.0	75	2 H69993	hypothetical prote
7	27	100.0	79	2 S76591	hypothetical prote
8	27	100.0	82	2 S02660	9K protein (clone
9	27	100.0	86	2 D83389	conserved hypothet
10	27	100.0	87	2 S07959	cytochrome b5, mic
11	27	100.0	87	2 T04413	probable narigenin
12	27	100.0	88	2 I40653	9K protein - Coxie
13	27	100.0	92	2 D70715	hypothetical prote
14	27	100.0	97	2 S53115	stilbene synthase
15	27	100.0	98	1 CBRH5E	cytochrome b5, ery
16	27	100.0	98	1 JN0316	cytochrome b5, ery
17	27	100.0	98	1 JC5783	cytochrome b5, ery
18	27	100.0	99	2 S56675	narigenin-chalcon
19	27	100.0	100	2 JC5596	cytochrome b5, bra
20	27	100.0	103	2 E86564	yldd family (impor
21	27	100.0	103	2 T20347	hypothetical prote
22	27	100.0	103	2 H72060	yldd family - Chla
23	27	100.0	105	2 C72608	hypothetical prote
24	27	100.0	106	2 E81606	conserved hypothet
25	27	100.0	108	2 T49518	hypothetical prote
26	27	100.0	112	2 S71324	cytochrome b5 - pl
27	27	100.0	114	2 T22905	hypothetical prote
28	27	100.0	116	2 S12557	19 heavy chain - h
29	27	100.0	118	2 G72610	hypothetical prote

30	27	100.0	120	2 S63052	cytochrome b5 - ye
31	27	100.0	121	2 H96631	probable Cytochrom
32	27	100.0	124	2 T40071	cytochrome b5 - fl
33	27	100.0	124	2 S20784	19 heavy chain V r
34	27	100.0	127	2 T37112	hypothetical prote
35	27	100.0	129	2 T41083	probable cytochrom
36	27	100.0	129	2 T36299	probable proline-r
37	27	100.0	132	2 E84905	probable cytochrom
38	27	100.0	133	2 CBRH05	cytochrome b5, mic
39	27	100.0	134	1 CBRH05	cytochrome b5, mic
40	27	100.0	134	1 CBRB5	cytochrome b5, mic
41	27	100.0	134	1 CBRB05	cytochrome b5, mic
42	27	100.0	134	1 CBRP5	cytochrome b5, mic
43	27	100.0	134	1 CBRP5	cytochrome b5, mic
44	27	100.0	134	2 T52469	cytochrome b5 (imp
45	27	100.0	134	2 T14454	cytochrome b5 - w1

ALIGNMENTS

RESULT 1
I51879
Cystathionine beta-synthase - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C:Accession: I51879
R:Sebastio, G.; Sperandio, M.P.; Panico, M.; de Franchis, R.; Kraus, J.P.; Andria, G.
Am. J. Hum. Genet. 56, 1324-1333, 1995
A:Title: The molecular basis of homocystinuria due to cystathionine beta-synthase def
A:Reference number: I51879; MUID:95282779
A:Accession: I51879
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: GB:S78267; NID:g999349; PIDN:AAB34404.1; PID:g999350

Query Match 100.0%; Score 27; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 HPGG 4
DB 6 HPGG 9
RESULT 2
A48158
Pheromone precursor MF alpha - fungus (Filobasidium floricorne)
C:Species: Filobasidiella neofornans, Cryptococcus neofornans
C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C:Accession: A48158
R:Moore, T.D.; Edman, J.C.
Mol. Cell. Biol. 13, 1962-1970, 1993
A:Title: The alpha-mating type locus of Cryptococcus neofornans contains a peptide ph
A:Reference number: A48158; MUID:93180845
A:Accession: A48158
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-38 <MOO>
A>Note: sequence inconsistent with nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBIN:126064, NCBIP:126070)

Query Match 100.0%; Score 27; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 HPGG 4
DB 28 HPGG 31

RESULT 3

PQ0816 probable cytochrome b5 - rape (fragment)

C:Species: Brassica napus (rape)

C:Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 20-Apr-2000

C:Accession: PQ0816

R:Park, Y.S.; Kwak, J.M.; Kwon, O.Y.; Kim, Y.S.; Lee, D.S.; Cho, M.J.; Lee, H.H.; Nam, H.

Plant Physiol. 103, 359-370, 1993

A:Title: Generation of expressed sequence tags of random root cDNA clones of Brassica napus

A:Reference number: PQ0816; MUID:94302145

A:Accession: PQ0816

A:Molecule type: mRNA

A:Residues: 1-51 <PAR>

A:Experimental source: root, cv. Naehan

A:Superfamily: cytochrome b5; cytochrome b5 core homology

F:1-51/Domain: cytochrome b5 core homology (fragment) <CB5>

Query Match

100.0%; Score 27; DB 2; Length 51;

Best Local Similarity 100.0%; Pred. No. 67;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4

DB 13 HPGG 16

RESULT 4

T05913 hypothetical protein - barley (fragment)

C:Species: Hordeum vulgare (barley)

C:Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 08-Oct-1999

C:Accession: T05913

R:Hess, W.R.; Golz, R.R.; Boerner, T.

Plant Sci. 133, 191-201, 1998

A:Title: Analysis of randomly selected cDNAs reveals the expression of stress- and defense

A:Reference number: 215411

A:Accession: T05913

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-64 <HES>

A:Cross-references: EMBL:AJ000237; NID:e1055248; PIDN:CAA03958.1; PID:e1312740

A:Experimental source: cv. Haisa, leaf

Query Match

100.0%; Score 27; DB 2; Length 64;

Best Local Similarity 100.0%; Pred. No. 82;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4

DB 46 HPGG 49

RESULT 5

AA1085 nitrate reductase (NADH) (EC 1.6.6.1) - curled-leaved tobacco (fragment)

C:Species: Nicotiana glauca (curled-leaved tobacco)

C:Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 11-Jun-1999

C:Accession: AA1085

R:Meyer, C.; Levin, J.M.; Roussel, J.M.; Rouze, P.

J. Biol. Chem. 266, 20561-20566, 1991

A:Title: Mutational and structural analysis of the nitrate reductase heme domain of Nicotiana

A:Reference number: AA1085; MUID:92041899

A:Accession: AA1085

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-74 <MEY>

A:Cross-references: GB:S61885; NID:9237968; PIDN:AA020155.1; PID:9237969

C:Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductase; cytochrome b5 core homology (fragment) <CB5>

F:42.65/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match

100.0%; Score 27; DB 2; Length 74;

Best Local Similarity 100.0%; Pred. No. 94;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4

DB 42 HPGG 45

RESULT 6

H69993 hypothetical protein YtjA - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

C:Accession: H69993

R:Kunst, F.; Ogatawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber

C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,

Nature 390, 249-256, 1997

A:Authors: Rouger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gal

lechi, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanl

A:Authors: Schleich, S.; Schoeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se

akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Tosato, V.; Uchiya

T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida

A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danclun, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis

A:Reference number: A69580; MUID:98044033

A:Accession: H69993

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-75 <RUN>

A:Cross-references: GB:299119; GB:AL009126; NID:92635411; PIDN:CA015046.1; PID:926355

A:Experimental source: strain 168

C:Genetics:

A:Gene: ytjA

C:Superfamily: conserved hypothetical protein H11000

Query Match

100.0%; Score 27; DB 2; Length 75;

Best Local Similarity 100.0%; Pred. No. 95;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4

DB 61 HPGG 64

RESULT 7

S76591 hypothetical protein - Synechocystis sp. (strain PCC 6803)

C:Species: Synechocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C:Accession: S76591

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,

O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

S:Reference number: S74322; MUID:97061201

A:Accession: S76591

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-79 <KAN>

A:Cross-references: EMBL:D64002; GB:AB001339; NID:q1001612; PIDN:BA10437.1; PID:q100

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Superfamily: conserved hypothetical protein HI1000

Query Match 100.0%; Score 27; DB 2; Length 79;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPGG 4
|||||
DB 62 HPGG 65

RESULT 8

9K protein (clone pc4) - human

C:Species: Homo sapiens (man)

C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jul-2000

C:Accession: S02660

R:Lammers, R.; Gross, G.; Mayr, U.; Collins, J.

Eur. J. Biochem. 178, 93-99, 1988

A:Title: Alternative mechanisms for gene activation induced by poly(ri) * poly(rc) and N

A:Reference number: S02660; MUID:89078418

A:Accession: S02660

A:Molecule type: mRNA

A:Residues: 1-82 <LMA>

A:Cross-references: EMBL:X13956; NID:g32574; PIDN:CAA32138.1; PID:g32575

Query Match 100.0%; Score 27; DB 2; Length 82;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPGG 4
|||||
DB 56 HPGG 59

RESULT 9

conserved hypothetical protein PA2045 [Imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: D83389

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Ladbis, K.; Lim,

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: A82950; MUID:20437337

A:Accession: D83389

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-86 <STC>

A:Cross-references: GB:AE004631; GB:AE004091; NID:g9948050; PIDN:AAG05433.1; GSPDB:GN001

A:Genetics:

A:Gene: PA2045

C:Superfamily: conserved hypothetical protein HI1000

C:Species: Alouatta fusca (brown howler monkey)

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-May-2000

C:Accession: S07959; A92077; A00167

R:Ozols, J.

Biochim. Biophys. Acta 997, 121-130, 1989

A:Title: Structure of cytochrome b(5) and its topology in the microsomal membrane.

A:Reference number: S04976; MUID:89323209

A:Accession: S07959

A:Molecule type: protein

A:Residues: 1-87 <OZO>

R:Nobrega, F.G.; Ozols, J.

J. Biol. Chem. 246, 1706-1717, 1971

A:Title: Amino acid sequences of tryptic peptides of cytochromes b-5 from microsomes

A:Reference number: A92077; MUID:71134790

A:Accession: A92077

A:Molecule type: protein

A:Residues: 1-10, 'Q', 12-13, 'E', 15-57, 'D', 59-74, 'Y', 76-84, 'K', 86, 'R' <NOB>

C:Superfamily: cytochrome b5; cytochrome b5 core homology

C:Keywords: electron transfer; heme; iron; liver; metalloprotein

F:5-80/Domain: cytochrome b5 core homology <CR5>

F:40,64/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 100.0%; Score 27; DB 2; Length 87;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPGG 4
|||||
DB 40 HPGG 43

RESULT 11

probable naringenin-chalcone synthase (EC 2.3.1.74) - barley (fragment)

C:Species: Hordeum vulgare (barley)

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000

C:Accession: T04413

R:Lee, J.E.; Parthier, B.; Loebler, M.

submitted to the EMBL Data Library, December 1995

A:Description: Jasmonate signalling can be uncoupled from ABA signalling in barley: 1

A:Reference number: Z15346

A:Accession: T04413

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-87 <LEE>

A:Cross-references: EMBL:U43494; NID:g1167949; PIDN:AAA87040.1; PID:g1167950

A:Experimental source: cv. Salome, leaf

C:Superfamily: chalcone synthase

C:Keywords: acyltransferase; coenzyme A; flavonoid biosynthesis

Query Match 100.0%; Score 27; DB 2; Length 87;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPGG 4
|||||
DB 6 HPGG 9

RESULT 12

9K protein - Coxiiella burnetii

C:Species: Coxiiella burnetii

C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 29-Sep-1999

C:Accession: I40653

R:Suhan, M.; Chen, S.Y.; Thompson, H.A.; Hoover, T.A.; Hill, A.; Williams, J.C.

J. Bacteriol. 176, 5233-5243, 1994

A:Title: Cloning and characterization of an autonomous replication sequence from CoxI

A:Reference number: I40647; MUID:94350801

A:Accession: I40653

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: protein

A:Residues: 1-87 <LEE>

A:Cross-references: EMBL:U43494; NID:g1167949; PIDN:AAA87040.1; PID:g1167950

A:Experimental source: cv. Salome, leaf

C:Superfamily: chalcone synthase

C:Keywords: acyltransferase; coenzyme A; flavonoid biosynthesis

Query Match 100.0%; Score 27; DB 2; Length 87;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPGG 4
|||||
DB 6 HPGG 9

RESULT 12

9K protein - Coxiiella burnetii

C:Species: Coxiiella burnetii

C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 29-Sep-1999

C:Accession: I40653

R:Suhan, M.; Chen, S.Y.; Thompson, H.A.; Hoover, T.A.; Hill, A.; Williams, J.C.

J. Bacteriol. 176, 5233-5243, 1994

A:Title: Cloning and characterization of an autonomous replication sequence from CoxI

A:Reference number: I40647; MUID:94350801

A:Accession: I40653

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: protein

A:Residues: 1-87 <LEE>

A:Cross-references: EMBL:U43494; NID:g1167949; PIDN:AAA87040.1; PID:g1167950

A:Experimental source: cv. Salome, leaf

C:Superfamily: chalcone synthase

C:Keywords: acyltransferase; coenzyme A; flavonoid biosynthesis

A:Molecule type: DNA
 A:Residues: 1-88 <RES>
 A:Cross-references: EMBL:U10529; NID:9511451; PIDN:AAA56918.1; PID:9511458
 C:Superfamily: conserved hypothetical protein H11000

Query Match 100.0%; Score 27; DB 2; Length 88;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
 ||||
 DB 73 HPGG 76

RESULT 13

D70715
 hypothetical protein RV0942 - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C:Accession: D70715
 R:Colo, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Genies, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellon, S.; Squares, S.
 Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987

A:Accession: D70715

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-92 <COL>

A:Cross-references: GB:Z79700; GB:AL123456; NID:93261628; PIDN:CAB01979.1; PID:e264107;

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: RV0942

Query Match 100.0%; Score 27; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
 ||||
 DB 66 HPGG 69

RESULT 14

S53315

stilbene synthase - grape

C:Species: Vitis sp. (grape)

C:Date: 14-Jul-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999

C:Accession: S53315

R:Wiese, W.; Vornam, B.; Krause, E.; Kindl, H.

Plant Mol. Biol. 26, 667-677, 1994

A:Title: Structural organization and differential expression of three stilbene synthase

A:Reference number: S53313; MUID:95036047

A:Accession: S53315

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-97 <NIE>

C:Superfamily: chalcone synthase

Query Match 100.0%; Score 27; DB 2; Length 97;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
 ||||
 DB 8 HPGG 11

RESULT 15

CBH05E

cytochrome b5, erythrocyte splice form [validated] - human

C:Species: Homo sapiens (man)

C:Date: 08-Aug-1987 #sequence_revision 05-Apr-1995 #text_change 20-Apr-2000

C:Accession: JN0075; B24211

R:Giordano, S.J.; Stegless, A.W.

Biochem. Biophys. Res. Commun. 178, 38-44, 1991

A:Title: The human liver and reticulocyte cytochrome b5 mRNAs are products from a sin

A:Reference number: JN0075; MUID:91298976

A:Accession: JN0075

A:Molecule type: mRNA

A:Residues: 1-98 <GIO>

A:Cross-references: GB:M60174; NID:9181391; PIDN:AAA52165.1; PID:9181392

A:Experimental source: erythrocyte

R:Abel, K.; Kimura, S.; Kizawa, R.; Anan, F.K.; Sugita, Y.

J. Biochem. 97, 1659-1668, 1985

A:Title: Amino acid sequences of cytochrome b5 from human, porcine, and bovine erythr

A:Reference number: A91992; MUID:85289161

A:Accession: B24211

A:Molecule type: protein

A:Residues: 2-88, 'K', '90', 'R', '92-98 <ABE>

A:Experimental source: erythrocyte

C:Comment: Cytochrome b5 exists in at least two alternative splice forms. This shorte

C:Genetics:

A:Gene: GDB:CYB5

A:Cross-references: GDB:125236; OMIM:250790

A:Map position: 18q23-18q23

A:Introns: 86/3

A:Note: the list of introns may be incomplete

C:Function:

A:Description: acts to reduce methemoglobin to functional hemoglobin; the oxidized fo

A:Note: a deficiency of this protein causes type IV hereditary methemoglobinemia

C:Superfamily: cytochrome b5; cytochrome b5 core homology

C:Keywords: acetylated amino end; alternative splicing; chromoprotein; electron trans

F;2-96/Product: cytochrome b5, erythrocyte splice form #status experimental <MAT>

F;9-84/Domains: cytochrome b5 core homology <CB5>

F;2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental

F;44/Binding site: heme iron (His) (axial ligands) #status predicted

QY 1 HPGG 4
 ||||
 DB 44 HPGG 47

Query Match 100.0%; Score 27; DB 1; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: August 9, 2001, 20:26:04
 J00 time: 243 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 9, 2001, 20:36:48 ; Search time 28.86 Seconds
(without alignments)
4.748 Million cell updates/sec

Title: US-09-367-013b-2_COPY_50_53

Perfect score: 27

Sequence: 1 HPGG 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	53	RL2A_PIG	Q29333 sus scrofa
2	27	100.0	55	ITRP_HALRO	P16589 halocynthia
3	27	100.0	82	1 9KD_HUMAN	P13994 homo sapien
4	27	100.0	85	1 YIDD_ECOLI	P22847 escherichia
5	27	100.0	87	1 CYB5_ALOSE	P00168 alouatta se
6	27	100.0	88	1 YIDD_COXBU	P45649 coxiella bu
7	27	100.0	92	1 Y942_MYCTU	P11567 mycobacteri
8	27	100.0	99	1 CHSY_FRAAN	P51076 fragaria an
9	27	100.0	120	1 CUI9_ARADI	P80515 araneus dia
10	27	100.0	120	1 CYB5_YEAST	P40312 saccharomyc
11	27	100.0	132	1 CYB5_BOROF	P04354 borago offi
12	27	100.0	133	1 CYB5_BOVIN	P00171 bos taurus
13	27	100.0	133	1 CYB5_HORSE	P00170 equus cabal
14	27	100.0	133	1 CYB5_HUMAN	P00167 homo sapien
15	27	100.0	133	1 CYB5_MOUSE	P56395 mus musculu
16	27	100.0	133	1 CYB5_PIG	P00172 sus scrofa
17	27	100.0	133	1 CYB5_RABIT	P00169 oryctolagus
18	27	100.0	133	1 CYB5_RAT	P00173 rattus norv
19	27	100.0	134	1 CY51_ARATH	Q42342 arabidopsis
20	27	100.0	134	1 CY52_ARATH	O48845 arabidopsis
21	27	100.0	134	1 CYB5_BRAOL	P40934 brassica ol
22	27	100.0	134	1 CYB5_MUSDO	P49096 musca domes
23	27	100.0	135	1 CYB5_CUSRE	P49097 cusculta ref
24	27	100.0	135	1 CYB5_TOBAC	P49099 nicotiana t
25	27	100.0	136	1 CYB5_TOBAC	P49098 nicotiana t
26	27	100.0	137	1 CYB5_ORYSA	P49100 oryza sativ
27	27	100.0	138	1 CYB5_CHICK	P00174 gallus gall
28	27	100.0	142	1 CYBR_DROVI	P50266 drosophila
29	27	100.0	145	1 RL13_BACSU	P01097a bacillus su
30	27	100.0	145	1 RL2A_OSCBR	O01338 oscineus br
31	27	100.0	146	1 AROF_STRLI	P55911 streptomyce
32	27	100.0	146	1 CYM5_HUMAN	O43169 homo sapien
33	27	100.0	146	1 CYM5_RAT	P04166 rattus norv

34	27	100.0	146	1 RL2A_ARATH	P49637 arabidopsis
35	27	100.0	147	1 RL2A_HUMAN	P46776 homo sapien
36	27	100.0	147	1 RL2A_RAT	P18445 rattus norv
37	27	100.0	147	1 RL2A_XENLA	P47830 xenopus lae
38	27	100.0	148	1 RL2A_SCHPO	P36585 schizosacch
39	27	100.0	148	1 RL2B_SCHPO	P37728 schizosacch
40	27	100.0	148	1 RL2B_YEAST	P22406 saccharomyc
41	27	100.0	148	1 RL2A_DICDI	P48160 dictyostell
42	27	100.0	148	1 RL2A_EUPCR	P48161 euploties cr
43	27	100.0	148	1 RL2A_TENMO	O27021 tenedrio mo
44	27	100.0	149	1 RL2B_NECR	P08978 neurospora
45	27	100.0	149	1 RL2B_DROME	Q94330 drosophila

ALIGNMENTS

RESULT 1	RL2A_PIG	STANDARD;	PRT;	53 AA.
AC	Q29333;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	605 RIBOSOMAL PROTEIN L27A (FRAGMENT).			
GN	RPL27A.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.			
OX	NCBI_TaxID:9823;			
RP	SEQUENCE FROM N.A.			
RN	[1]			
RC	TISSUE=Small intestine;			
RX	MEDLINE=96327607; PubMed=8672129;			
RA	Winteroe A.K., Fredholm M., Davies W.;			
RT	"Evaluation and characterization of a porcine small intestine cDNA			
RL	library: analysis of 839 clones.";			
CC	Mamm. Genome 7:509-517(1996).			
CC	-I- SIMILARITY: BELONGS TO THE L15P FAMILY OF RIBOSOMAL PROTEINS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	-----			
DR	EMBL; F14739; CAA23218.1; -			
DR	InterPro; IPR001196; -			
DR	PROSITE; PS00475; RIBOSOMAL_L15; PARTIAL.			
KW	Ribosomal protein.			
FT	INIT_MET 0			
FT	NON_TER 53			
FT	BY SIMILARITY.			
SQ	SEQUENCE 53 AA; 6050 MW; 2FEE757B074BE7E CRC64;			
Query Match	100.0%; Score 27; DB 1; Length 53;			
Best Local Similarity	100.0%; Pred. No. 34;			
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
OY	1 HPGG 4			
DB	27 HPGG 30			
RESULT 2	ITRP_HALRO	STANDARD;	PRT;	55 AA.
AC	P16589;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	01-FEB-1995 (Rel. 31, Last annotation update)			

DE TRYPSIN INHIBITOR.
 OS Halocynthia roretzi (Sea squirt).
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
 OC Stolidobranchia; Pyuridae; Halocynthia.
 OX NCB1_TaxID=7729;
 RN [1]
 RP SEQUENCE:
 RC TISSUE=Hemolymph; PubMed-2341375;
 RX MEDLINE=90256715; PubMed-2341375;
 RA Kumazaki T., Hoshiba N., Yokosawa H., Ishii S.-I.;
 RT "Primary structure of ascidian trypsin inhibitors in the hemolymph of
 a solitary ascidian, Halocynthia roretzi.";
 RL J. Biochem. 107:409-413(1990).
 RN [2]
 RP DISULFIDE BONDS.
 RX MEDLINE=90256716; PubMed-2111316;
 RA Kumazaki T., Ishii S.-I.;
 RT "Disulfide bridge structure of ascidian trypsin inhibitor I:
 similarity to Kazal-type inhibitors.";
 RL J. Biochem. 107:414-419(1990).
 CC -1- FUNCTION: POTENT INHIBITOR OF TRYPSIN.
 CC -1- SIMILARITY: SOME TOPOLOGICAL SIMILARITY TO KAZAL-TYPE INHIBITORS.
 KM Serine protease inhibitor; Hemolymph.
 FT DISULFID 5 40
 FT DISULFID 12 41
 FT DISULFID 14 37
 FT DISULFID 23 54
 FT ACT SITE 16 17 REACTIVE BOND.
 SQ SEQUENCE 55 AA; 6078 MW; 4121548DB33207C2 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 55;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPGC 4
 DB 43 HPGC 46

RESULT 3
 9KD_HUMAN STANDARD; PRT; 82 AA.
 ID P13994;
 DT 01-JAN-1990 (rel. 13, Created)
 DT 01-JAN-1990 (rel. 13, Last sequence update)
 DT 01-OCT-2000 (rel. 40, Last annotation update)
 DE 9 KDA PROTEIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo; PubMed-3203696;
 RX MEDLINE=89078418; PubMed-3203696;
 RA Lamers R., Gross G., Mayr U., Collins J.;
 RT "Alternative mechanisms for gene activation induced by
 poly(rl).poly(rl) and Newcastle disease virus.";
 RL Eur. J. Biochem. 178:93-99(1988).
 CC -1- INDUCTION: BY POLY(RL), POLY(RC) AND NEWCASTLE DISEASE VIRUS.
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 DR EMBL: X13956; CAA2138.1; -
 DR PIR: S02660; S02660.
 SQ SEQUENCE 82 AA; 8594 MW; 984A1552A489652 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 82;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPGC 4
 DB 56 HPGC 59

RESULT 4
 YIID_ECOLI STANDARD; PRT; 85 AA.
 ID YIID_ECOLI
 AC P22847;
 DT 01-AUG-1991 (rel. 19, Created)
 DT 01-AUG-1991 (rel. 19, Last sequence update)
 DT 01-NOV-1997 (rel. 35, Last annotation update)
 DE HYPOTHETICAL 9.4 KDA PROTEIN IN RNPA-THDF INTERGENIC REGION.
 GN YIID.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCB1_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86056995; PubMed-2415431;
 RA Hansen F.G., Hansen E.B., Allung T.;
 RT "Physical mapping and nucleotide sequence of the rnpA gene that
 RT encodes the protein component of ribonuclease P in Escherichia
 RT coli.";
 RL Gene 38:85-93(1985).
 CC -1- SIMILARITY: NO THE CORRESPONDING ORF IN RELATED BACTERIA.
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 DR EMBL: M1056; -; NOT_ANNOTATED_CDS.
 DR Ecogene: EG11348; YIID.
 DR InterPro: IPR002696; -
 DR Pfam: PF01809; DUF37; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 85 AA; 9381 MW; DCD2A8E612D12348 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 85;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPGC 4
 DB 68 HPGC 71

RESULT 5
 CYB5_ALOSE STANDARD; PRT; 87 AA.
 ID CYB5_ALOSE
 AC P00168;
 DT 21-JUL-1986 (rel. 01, Created)
 DT 01-OCT-1989 (rel. 12, Last sequence update)
 DT 01-OCT-2000 (rel. 40, Last annotation update)
 DE CYTOCHROME B5 (FRAGMENT).
 GN CYB5.
 OS Alouatta seniculus (Howler monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Alouattinae;
 OX NCB1_TaxID=9503;

```

RN [1]
RP MEDLINE=71134790; PubMed=4993957;
RX Nobrega F.G., Ozols J.;
RT "Amino acid sequences of tryptic peptides of cytochromes b5 from
RL microsomes of human, monkey, porcine, and chicken liver.";
RN [2]
RP MEDLINE=8933209; PubMed=2752049;
RX Ozols J.;
RT "Structure of cytochrome b5 and its topology in the microsomal
RL membrane.";
RL Biochim. Biophys. Acta 997:121-130(1989).
CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CC OXYGENASES.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE. BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC PIR: A00167; CBHUS.
CC PIR: S07959; S07959.
CC HSSP: P00171; 3BSC.
CC DR InterPro: IPR001199; -.
CC DR Pfam: PF001173; heme_1; 1.
CC DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
CC DR PROSITE: PS0255; CYTOCHROME_B5_2; 1.
CC KM Electron transport; Membrane; Heme; Microsome.
FT BINDING 40 40 HEME LIGAND (BY SIMILARITY).
FT BINDING 64 64 HEME LIGAND (BY SIMILARITY).
FT CONFLICT 11 14 HEI0 -> OEIE (IN REF. 1).
FT CONFLICT 85 87 RPK -> KPR (IN REF. 1).
FT NON_TER 87 87
SO SEQUENCE 87 AA; 10032 MW; 5B3552315D1A0F5C CRC64;

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Query Match 100.0%; Score 27; DB 1; Length 87;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
   ||||
Db 40 HPGG 43

RESULT 6
YIDD_CXBU STANDARD; PRT; 88 AA.
ID YIDD_CXBU
AC P45649;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE HYPOTHETICAL 9.9 KDA PROTEIN IN RNPA 3 REGION.
OS Coxiella burnetii.
OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
CC Coxiella group; Coxiella.
OX NCBI_TaxID=777;
RX MEDLINE=94350801; PubMed=8071197;
RA Suhm M., Chen S.Y., Thompson H.A., Hoover T.A., Hill A.,
RA Williams J.C.;
RT "Cloning and characterization of an autonomous replication sequence
RL from Coxiella burnetii.";
RT J. Bacteriol. 176:5233-5243(1994).
CC -1- SIMILARITY: TO THE CORRESPONDING ORF IN RELATED BACTERIA.
CC -----
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CC -----
DR EMBL: U10529; AAA56918.1; -.
DR InterPro: IPR002696; -.
DR Pfam: PF01809; DUF37; 1.
KW Hypothetical protein.
SQ SEQUENCE 88 AA; 9923 MW; 9A2F3A1C0734501D CRC64;

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```

Query Match 100.0%; Score 27; DB 1; Length 88;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
   ||||
Db 73 HPGG 76

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```

RESULT 7
Y942_MYCTU STANDARD; PRT; 92 AA.
ID Y942_MYCTU
AC P71567;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HYPOTHETICAL 9.7 KDA PROTEIN RV0942.
GN RV0942 OR MYCT10D7.32C.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RX Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RX Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RX Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RX Davies R., Devlin K., Feltham T., Gentles S., Hamlin N., Holroyd S.,
RX Horvath T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RX Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RX Rutter S., Seeger K., Skellon S., Squares S., Squares R., Sulston J.E.,
RX Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
CC -----
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CC -----
DR EMBL: Z79700; CAB01979.1; -.
DR TuberculList; RV0942; -.
KW Hypothetical protein.
SQ SEQUENCE 92 AA; 9737 MW; F0732A4A607D47C6 CRC64;

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Query Match 100.0%; Score 27; DB 1; Length 92;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
   ||||
Db 66 HPGG 69

RESULT 8
CHSY_FRAAN

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```

ID CHSY_FRAAN STANDARD; PRT; 99 AA.
AC P51076;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CHALCONE SYNTHASE RJ5 (EC 2.3.1.74) (NARINGENIN-CHALCONE SYNTHASE)
DE (FRAGMENT).
OS Fragaria ananassa (Strawberry).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Rosales; Rosaceae; Fragaria.
ON NCBI_TaxId=3747;
RX STRAIN=CV. PAJARO; TISSUE=Fruit;
RX MEDLINE=95284359; PubMed=7766892;
RA Wilkinson J.O., Lanahan M.B., Conner T.W., Klee H.J.;
RT Identification of mRNAs with enhanced expression in ripening
RT strawberry fruit using polymerase chain reaction differential
RT display.
RL Plant Mol. Biol. 27:1097-1108(1995).
CC -1- FUNCTION: THE PRIMARY PRODUCT OF THIS ENZYME IS 4,2',4',6'-
CC TETRAHYDROXYCHALCONE (ALSO TERMED NARINGENIN-CHALCONE OR CHALCONE)
CC WHICH CAN UNDER SPECIFIC CONDITIONS SPONTANEOUSLY ISOMERIZE INTO
CC NARINGENIN.
CC -1- CATALYTIC ACTIVITY: 3 MALONYL-COA + 4-COUMAROYL-COA = 4 COA +
CC NARINGENIN-CHALCONE + 3 CO(2)
CC -1- PATHWAY: PART OF THE BIOSYNTHETIC PATHWAY FOR ALL CLASSES OF
CC FLAVONOIDS, A LARGE CLASS OF SECONDARY PLANT METABOLITES, MANY
CC OF WHICH ARE BRIGHTLY COLORED.
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY IN DEVELOPING FRUIT.
CC -1- DEVELOPMENTAL STAGE: EXPRESSION OF THE PROTEIN IS ENHANCED IN A
CC RIPENING FRUIT.
CC -1- SIMILARITY: BELONGS TO THE CHALCONE/STILBENE SYNTHASES FAMILY.
CC
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CC
CC EMBL: U19942; AAA79923.1; -
CC InterPro: IPR001099; -
CC pfam: PR00195; Chal_stil_synth.1.
CC PROSITE: PS00441; CHALCONE_SYNTH; PARTIAL.
CC Flavonoid biosynthesis; Transferase; Acyltransferase.
CC NON_TER 1
CC SEQUENCE 99 AA; 10715 MW; 38F83BA5F6B1179B CRC64;
SQ

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Query Match 100.0%; Score 27; DB 1; Length 99;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 HPGG 4
    ||||
DB 13 HPGG 16

```

RESULT 9
 CUI9_ARADI STANDARD; PRT; 120 AA.
 AC P80515;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 36, Last annotation update)
 DE ADULT-SPECIFIC RIGID CUTICULAR PROTEIN 11.9 (ACP 11.9).
 OS Araneus diadematus (Spider).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Araneomorphae; Entelegynae; Araneidae; Araneidae; Araneus.
 ON NCBI_TaxId=45920;
 CC

```

RN [1]
RP SEQUENCE.
RC TISSUE-Cuticle;
RX MEDLINE=97166616; PubMed=9014336;
RA Norup T., Berg T., Stenholm H., Andersen S.O., Hoejrup P.;
RT "Purification and characterization of five cuticular proteins from
RT the spider Araneus diadematus."
RL Insect Biochem. Mol. Biol. 26:907-915(1996).
CC -1- FUNCTION: COMPONENT OF THE RIGID CUTICLE OF THE SPIDER.
CC -1- MASS SPECTROMETRY: MW=11872.1; METHOD-ELECTROSPRAY.
CC -1- SIMILARITY: CONTAINS A CUTICLE CONSENSUS DOMAIN.
CC
CC HSSP: P04002; IATP.
CC InterPro: IPR000618; -
CC pfam: PR00379; Insect_cuticle; 1.
CC PRINTS: PR00947; CUTICLE.
CC PROSITE: PS00233; CUTICLE; 1.
CC Structural protein; Cuticle.
CC DOMAIN 73
CC SEQUENCE 120 AA; 11871 MW; 8D3E577C61999DC2 CRC64;
SQ

```

Query Match 100.0%; Score 27; DB 1; Length 120;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 HPGG 4
    ||||
DB 112 HPGG 115

```

RESULT 10
 CYB5_YEAST STANDARD; PRT; 120 AA.
 AC P40312;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CYTOCHROME B5.
 GN CYB5 OR YNL11C OR N1949.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 ON NCBI_TaxId=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PL100;
 RX MEDLINE=94237477; PubMed=8181746;
 RA Truan G., Epinat J.-C., Rougeulle C., Cullin C., Pompon D.;
 RT "Cloning and characterization of a yeast cytochrome b5-encoding gene
 RT which suppresses ketoconazole hypersensitivity in a MDPH-P-450
 RT reductase-deficient strain.";
 RL Gene 142:123-127(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9745296; PubMed=9090055;
 RA de Antoni A., D'Angelo M., Dal Pero F., Sartorello F., Pandolfo D.,
 RA Pallavicini A., Lanfranchi G., Valle G.;
 RT "The DNA sequence of cosmid 14-13b from chromosome XIV of
 RT Saccharomyces cerevisiae reveals an unusually high number of
 RT overlapping open reading frames.";
 RL Yeast 13:261-266(1997).
 CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
 CC OXYGENASES. IT PLAYS A ROLE IN FATTY-ACID DESATURATION AND IS ALSO
 CC INVOLVED IN SEVERAL STEPS OF THE STEROL BIOSYNTHESIS PATHWAY,
 CC PARTICULARLY IN THE 4-DEMETHYLATION OF THE 4,4'-DIMETHYL
 CC ZYMOSTEROL.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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DR EMBL; L22494; AAA67468.1; -
DR EMBL; Z69382; CAA93396.1; -
DR EMBL; Z71387; CAA95990.1; -
DR PIR; S47919; S47919.
DR HSSP; P04166; 1B5M.
DR SCD; S0005055; CYB5.
DR InterPro; IPR001199; -
DR Pfam; PF00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROME_B5.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KM Electron transport; Transmembrane; Heme; Microsome.
FT BINDING 37 37 HEME LIGAND (BY SIMILARITY).
FT BINDING 61 61 HEME LIGAND (BY SIMILARITY).
FT TRANSMEM 98 118 POTENTIAL.
FT CONFLICT 17 17 E -> O (IN REF. 1).
SQ SEQUENCE 120 AA; 13297 MW; 598EF2A6730CAD19 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
Db 37 HPGG 40

RESULT 11
ID CYB5_BOROF STANDARD; PRT; 132 AA.
AC 004354;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CYTOCHROME B5.
OS Borago officinalis (Borraghe) (Borage).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC euasterids I; incertae sedis; Boraginaceae; Borago.
OX NCBI_TaxID=13363;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268723; Pubmed=9108131;
RA Sayanova O., Smith M.A., Lapinskas P.A., Stobart K., Dobson G.,
RA Christie W.W., Shewry P.R., Napier J.A.;
RT "Expression of a borago desaturase cDNA containing an N-terminal
RT cytochrome b5 domain results in the accumulation of high levels of
RT delta6-desaturated fatty acids in transgenic tobacco.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
CC OXYGENASES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE, BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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DR EMBL; U79011; AAC49701.1; -
DR HSSP; P00171; ICYO.

DR Mendel; 15843; Borof; 1218; 15843.
DR InterPro; IPR001199; -
DR Pfam; PF00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROME_B5.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KM Electron transport; Transmembrane; Heme; Microsome.
FT BINDING 37 37 HEME LIGAND (BY SIMILARITY).
FT BINDING 61 61 HEME LIGAND (BY SIMILARITY).
FT TRANSMEM 104 124 POTENTIAL.
SQ SEQUENCE 132 AA; 14556 MW; 96EF72A06F2E8C5B CRC64;

Query Match 100.0%; Score 27; DB 1; Length 132;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
Db 37 HPGG 40

RESULT 12
ID CYB5_BOVIN STANDARD; PRT; 133 AA.
AC P00171; Q28837; Q27947;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CYTOCHROME B5.
GN CYB5.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89128451; Pubmed=2915932;
RA Cristiano R.J., Steggle A.W.;
RT "The complete nucleotide sequence of bovine liver cytochrome b5
RT mRNA.";
RL Nucleic Acids Res. 17:799-799(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver.
RX MEDLINE=94010928; Pubmed=8406485;
RA Cristiano R.J., Giordano S.J., Steggle A.W.;
RT "The isolation and characterization of the bovine cytochrome b5 gene,
RT and a transcribed pseudogene.";
RL Genomics 17:348-354(1993).
RN [3]
RP SEQUENCE OF 1-97.
RC TISSUE=Erythrocyte;
RX MEDLINE=85289161; Pubmed=4030743;
RA Abe K., Kimura S., Kizawa R., Anan F.K., Sugita Y.;
RT "Amino acid sequences of cytochrome b5 from human, porcine, and
RT bovine erythrocytes and comparison with liver microsomal cytochrome
RT b5.";
RL J. Biochem. 97:1659-1668(1985).
RN [4]
RP SEQUENCE OF 1-10 AND 130-133.
RX MEDLINE=74080219; Pubmed=4810060;
RA Ozols J.;
RT "Cytochrome b5 from microsomal membranes of equine, bovine, and
RT porcine livers. Isolation and properties of preparations containing
RT the membranous segment.";
RL Biochemistry 13:426-434(1974).
RN [5]
RP SEQUENCE OF 5-96.
RX MEDLINE=70067001; Pubmed=5391285;
RA Ozols J., Stultmatter P.;
RT "Correction of the amino acid sequence of calf liver microsomal

RT cytochrome b5." ;
 RN J. Biol. Chem. 244:6617-6618(1969).
 [6]
 RP SEQUENCE OF 5-95.
 RX MEDLINE=70289989; PubMed=5272324;
 RA Tsugita A., Kodayashi M., Tani S., Kyo S., Rashid M.A., Yoshida Y.,
 RA Kajihara T., Hagihara B.;
 RT "Comparative study of the primary structures of cytochrome b5 from
 RT four species." ;
 RL Proc. Natl. Acad. Sci. U.S.A. 67:442-447(1970).
 [7]
 RP SEQUENCE OF 91-133.
 RX MEDLINE=78218214; PubMed=670203;
 RA Fleming P.J., Dailey H.A., Corcoran D., Strittmatter P.;
 RT "The primary structure of the nonpolar segment of bovine cytochrome
 RT b5." ;
 RL J. Biol. Chem. 253:5369-5372(1978).
 [8]
 RP SEQUENCE OF 1-10.
 RX MEDLINE=89323209; PubMed=2752049;
 RA Ozols J.;
 RT "Structure of cytochrome b5 and its topology in the microsomal
 RT membrane." ;
 RL Biochim. Biophys. Acta 997:121-130(1989).
 [9]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF OXIDIZED FORM.
 RA Mathews F.S., Argos P., Levine M.;
 RT "The structure of cytochrome b-5 at 2.0-A resolution." ;
 RL Cold Spring Harb. Symp. Quant. Biol. 37:387-395(1971).
 [10]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF REDUCED FORM.
 RX MEDLINE=75095526; PubMed=1167544;
 RA Argos P., Mathews F.S.;
 RT "The structure of ferriocytochrome b5 at 2.8-A resolution." ;
 RL J. Biol. Chem. 250:747-751(1975).
 [11]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
 RA Durlley R.C.E., Mathews F.S.;
 RT "Refinement and structural analysis of bovine cytochrome b5 at 1.5-A
 RT resolution." ;
 RL Acta Crystallogr. D 52:65-76(1996).
 [12]
 RP STRUCTURE BY NMR.
 RX MEDLINE=96200988; PubMed=8613986;
 RA Muskett F.W., Kelly G.P., Whitford D.;
 RT "The solution structure of bovine ferricytochrome b5 determined using
 RT heteronuclear NMR methods." ;
 CC J. Mol. Biol. 258:172-189(1996).
 CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
 CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
 CC OXYGENASES.
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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 CC -----
 CC EMBL: X13617; CAA1949.1; -
 DR EMBL: M63328; AAC14455.1; ALT-SEQ.
 DR EMBL: M63326; AAC14455.1; JOINED.
 DR EMBL: M63327; AAC14455.1; JOINED.
 DR EMBL: I22966; -; NOT_ANNOTATED_CDS.
 DR PIR: A00170; CBBO5.
 DR PIR: F24211; F24211.
 DR PIR: S03428; S03428.
 DR PIR: S07963; S07963.
 DR PDB: 1CYO; 15-MAR-00.

DR PDB: 1MDB; 11-JAN-97.
 DR InterPro: IPR001199; -.
 DR Pfam: PF00173; heme_1; 1.
 DR PRINTS: PR00363; CYTOCHROME_B5.
 DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE: PS02555; CYTOCHROME_B5_2; 1.
 KW Electron transport; Transmembrane; Heme; Microsome; Acetylation;
 KW 3D-structure.
 FT INIT_MET 0 0
 FT MOD_RES 1 1
 FT DOMAIN 1 90
 FT BINDING 91 133
 FT BINDING 43 43
 FT BINDING 67 67
 FT CONFLICT 1 4
 FT CONFLICT 15 17
 FT CONFLICT 15 17
 FT CONFLICT 61 61
 FT CONFLICT 97 97
 FT CONFLICT 133 133
 FT STRAND 10 11
 FT HELIX 13 16
 FT TURN 17 18
 FT STRAND 20 21
 FT TURN 22 23
 FT STRAND 24 29
 FT TURN 30 31
 FT STRAND 32 35
 FT TURN 37 42
 FT TURN 44 45
 FT HELIX 48 51
 FT TURN 52 55
 FT STRAND 57 57
 FT HELIX 59 64
 FT TURN 65 66
 FT HELIX 69 75
 FT TURN 76 77
 FT STRAND 79 83
 FT HELIX 85 90
 SQ SEQUENCE 133 AA; 15198 MW; E27B60061E0BC43 CRC64;
 Query Match 100.0%; Score 27; DB 1; Length 133;
 Best Local Similarity 100.0%; Pred. No. 78;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HPGG 4
 DB 43 HPGG 46
 RESULT 13
 ID CYB5_HORSE STANDARD; PRT: 133 AA.
 AC P00170;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CYTOCHROME B5.
 GN CYB5.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OC NCBI_Taxid=9796;
 RN [1]
 RP SEQUENCE OF 1-98.
 RX MEDLINE=7028943; PubMed=977596;
 RA Ozols J., Gerard C., Nobrega F.G.;
 RT "Proteolytic cleavage of horse liver cytochrome b5. Primary structure
 RT of the heme-containing moiety." ;
 RL J. Biol. Chem. 251:6767-6774(1976).
 RN [2]
 RP SEQUENCE OF 89-133.
 RX MEDLINE=78045981; PubMed=562879;

RA Ozols J., Gerard C.;
 RT "Covalent structure of the membranous segment of horse cytochrome b5.
 RT Chemical cleavage of the native hemoprotein.";
 RL J. Biol. Chem. 252:8549-8553(1977).
 RN [3]
 RP SEQUENCE OF 1-10.
 RX MEDLINE=89323209; PubMed=2752049;
 RA Ozols J.;
 RT "Structure of cytochrome b5 and its topology in the microsomal
 RT membrane.";
 RL Biochim. Biophys. Acta 997:121-130(1989).
 CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
 CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
 CC OXYGENASES.
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR PIR; A29196; CBH05.
 DR PIR; S07964; S07964.
 DR HSSP; P00171; 1CYO.
 DR InterPro: IPR001199; -.
 DR Pfam: PF00173; heme_1; 1.
 DR PRINTS; PR00363; CYTOCHROMEBS.
 DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Electron transport; Transmembrane; Heme; Microsome; Acetylation.
 FT MOD_RES 1 1 ACETYLATION.
 FT DOMAIN 1 90 MEMBRANE-BINDING.
 FT BINDING 43 43 HEME LIGAND (BY SIMILARITY).
 FT BINDING 67 67 HEME LIGAND (BY SIMILARITY).
 FT CONFLICT 1 5 AEOSD -> ZEDAS (IN REF. 1).
 SO SEQUENCE 133 AA; 15140 MW; 85E50818D8CF4247 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 133;
 Best Local Similarity 100.0%; Pred. No. 78;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPGG 4
 DB 43 HPGG 46
 RESULT 14
 CYB5_HUMAN STANDARD; PRT; 133 AA.
 ID CYB5_HUMAN STANDARD; PRT; 133 AA.
 AC P00167;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CYTOCHROME B5.
 GN CYB5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89025904; PubMed=3178851;
 RT Yoo M., Steggle A.W.;
 RT "The complete nucleotide sequence of human liver cytochrome b5 mRNA.";
 RL Biochem. Biophys. Res. Commun. 156:576-580(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Li X.R., Giordano S.J., Yoo M., Steggle A.W.;
 RA Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 1-97 FROM N.A.
 RC TISSUE=Erythrocyte;
 RX MEDLINE=91298976; PubMed=1712589;
 RA Giordano S.J., Steggle A.W.;

RT "The human liver and reticulocyte cytochrome b5 mRNAs are products
 RT from a single gene.";
 RL Biochem. Biophys. Res. Commun. 178:38-44(1991).
 RN [4]
 RP SEQUENCE OF 1-97.
 RC TISSUE=Erythrocyte;
 RX MEDLINE=85289161; PubMed=4030743;
 RA Ade K., Kimura S., Kizawa R., Anan F.K., Sugita Y.;
 RT "Amino acid sequences of cytochrome b5 from human, porcine, and
 RT bovine erythrocytes and comparison with liver microsomal cytochrome
 RT b5.";
 RL J. Biochem. 97:1659-1668(1985).
 RN [5]
 RP SEQUENCE OF 1-90.
 RX MEDLINE=71134790; PubMed=4939357;
 RA Nobrega F.G., Ozols J.;
 RT "Amino acid sequences of tryptic peptides of cytochromes b5 from
 RT microsomes of human, monkey, porcine, and chicken liver.";
 RL J. Biol. Chem. 246:1706-1717(1971).
 RN [6]
 RP SEQUENCE OF 1-90.
 RX MEDLINE=72154531; PubMed=5062820;
 RA Ozols J.;
 RT "Cytochrome b5 from a normal human liver. Isolation and the partial
 RT amino acid sequence.";
 RL J. Biol. Chem. 247:2242-2245(1972).
 RN [7]
 RP SEQUENCE OF 1-90.
 RX MEDLINE=74074962; PubMed=4770377;
 RA Rashid M.A., Hagihara B., Kobayashi M., Tani S., Tsugita A.;
 RT "Structural studies of cytochrome b5. 3. Sequential studies on human
 RT liver cytochrome b5.";
 RL J. Biochem. 74:985-1002(1973).
 RN [8]
 RP SEQUENCE OF 1-35 AND 83-133.
 RX MEDLINE=89323209; PubMed=2752049;
 RA Ozols J.;
 RT "Structure of cytochrome b5 and its topology in the microsomal
 RT membrane.";
 RL Biochim. Biophys. Acta 997:121-130(1989).
 CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
 CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
 CC OXYGENASES.
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE (LIVER FORM). BOUND TO
 CC THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM. OR CYTOPLASMIC
 CC (ERYTHROCYTE FORM).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LIVER/MEMBRANE-BOUND FORM
 CC (SHOWN HERE) AND A ERYTHROCYTE/CYTOPLASMIC FORM; ARE PRODUCED BY
 CC ALTERNATIVE SPLICING.
 CC -1- DISEASE: DEFECTS IN CYB5 ARE THE CAUSE OF TYPE IV HEREDITARY
 CC METHEMOGLOBINEMIA.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 CC -----
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 CC -----
 DR EMBL; M22865; AAA35729.1; -;
 DR EMBL; L38945; AAA63169.1; ALT-SEQ.
 DR EMBL; L38792; AAA63169.1; JOINED.
 DR EMBL; L39941; AAA63169.1; JOINED.
 DR EMBL; L39942; AAA63169.1; JOINED.
 DR EMBL; L39943; AAA63169.1; JOINED.
 DR EMBL; L39944; AAA63169.1; JOINED.
 DR EMBL; M60174; AAA52165.1; -;
 DR PIR; A00167; CBH05.
 DR PIR; A28936; A28936.
 DR PIR; B24211; B24211.
 DR PIR; S04976; S04976.

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DR HSSP: P00171; 1MDB.
DR MIM: 250790; -.
DR InterPro: IPR001199; -.
DR pfam: PR00173; heme_1; 1.
DR PRINTS: PR00363; CYTOCHROME_B5_1; 1.
DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
DR Electron transport; Transmembrane; Heme; Microsome; Acetylation;
KW Alternative splicing.
FT INIT MET 0
FT MOD_RES 1
FT DOMAIN 1 90 ACETYLATION.
FT BINDING 91 133 MEMBRANE-BINDING.
FT BINDING 43 43 HEME LIGAND (BY SIMILARITY).
FT BINDING 67 67 HEME LIGAND (BY SIMILARITY).
FT VARSPPLIC 97 97 T -> P (IN ERYTHROCYTE ISOFORM).
FT VARSPPLIC 98 133 MISSING (IN ERYTHROCYTE ISOFORM).
FT CONFLICT 1 3 MISSING (IN REF. 5).
FT CONFLICT 3 3 O -> E (IN REF. 8).
FT CONFLICT 14 17 EEIQ -> OEIE (IN REF. 5, 6 AND 7).
FT CONFLICT 21 21 MISSING (IN REF. 7).
FT CONFLICT 61 61 N -> D (IN REF. 5, 6 AND 7).
FT CONFLICT 88 90 RPK -> KRR (IN REF. 4, 5, 6 AND 7).
FT CONFLICT 121 121 A -> V (IN REF. 8).
SQ SEQUENCE 133 AA; 15199 MW; 2FAD2AE87B6C992E CRC64;

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Query Match      100.0%; Score 27; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HPGG 4
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DB 43 HPGG 46

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DR EMBL: AA107504; -; NOT_ANNOTATED_CDS.
DR EMBL: W62851; -; NOT_ANNOTATED_CDS.
DR EMBL: AA106561; -; NOT_ANNOTATED_CDS.
DR EMBL: AA107511; -; NOT_ANNOTATED_CDS.
DR EMBL: AA086847; -; NOT_ANNOTATED_CDS.
DR EMBL: AA105541; -; NOT_ANNOTATED_CDS.
DR HSSP: P00173; 1AQA.
DR SWISS-2DPAGE: P56395; MOUSE.
DR InterPro: IPR001199; -.
DR pfam: PR00173; heme_1; 1.
DR PRINTS: PR00363; CYTOCHROME_B5_1; 1.
DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KW Electron transport; Transmembrane; Heme; Microsome.
FT INIT MET 0
FT DOMAIN 1 90 HEME-BINDING (BY SIMILARITY).
FT BINDING 91 133 MEMBRANE-BINDING (BY SIMILARITY).
FT BINDING 43 43 HEME LIGAND (BY SIMILARITY).
FT BINDING 67 67 HEME LIGAND (BY SIMILARITY).
SQ SEQUENCE 133 AA; 15110 MW; 5B540A370B38CEAE CRC64;

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Query Match      100.0%; Score 27; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HPGG 4
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DB 43 HPGG 46

Search completed: August 9, 2001, 20:36:48
Job time: 697 sec

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RESULT 15
CYB5_MOUSE STANDARD: PRT; 133 AA.
AC P56395:
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CYTOCHROME B5.
GN CYB5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,
RA Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,
RA Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B.,
RA Theisling B., Wylie T., Lennon G., Soares B., Wilson R., Waterston R.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
CC OXYGENASES. IT IS ALSO INVOLVED IN SEVERAL STEPS OF THE STEROL
CC BIOSYNTHESIS PATHWAY, PARTICULARLY IN THE C-5 DOUBLE BOND
CC INTRODUCTION DURING THE C-5 DESATURATION.
CC -!- SUBCELLULAR LOCATION: MICROSOmal MEMBRANE. BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC -----
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OM protein - protein search, using sw model

Run on: August 9, 2001, 20:36:14 ; Search time 87.05 Seconds
(without alignments)
6.079 Million cell updates/sec

Title: US-09-367-013b-2_COPY_50_53

Perfect score: 27
Sequence: 1 HPGG 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_16:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_prodent:*
12: sp_unclassified:*
13: sp_virtebrate:*
14: sp_virus:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	16	4 Q16350	Q16350 homo sapien
2	27	100.0	22	3 Q9UR51	Q9UR51 fillobasidie
3	27	100.0	22	3 Q9UR41	Q9UR41 fillobasidie
4	27	100.0	23	4 Q9UC01	Q9UC01 homo sapien
5	27	100.0	27	6 Q9TU40	Q9TU40 mammulthus p
6	27	100.0	27	6 Q9TU39	Q9TU39 elephas max
7	27	100.0	33	3 Q9HF31	Q9HF31 fillobasidie
8	27	100.0	33	3 Q9HF29	Q9HF29 fillobasidie
9	27	100.0	33	3 Q9HF28	Q9HF28 cryptococcu
10	27	100.0	33	3 Q9HF27	Q9HF27 cryptococcu
11	27	100.0	33	3 Q9HF26	Q9HF26 cryptococcu
12	27	100.0	33	3 Q9HF25	Q9HF25 cryptococcu
13	27	100.0	33	3 Q9HDP1	Q9HDP1 fillobasidie
14	27	100.0	33	3 Q9HDP0	Q9HDP0 cryptococcu
15	27	100.0	33	3 Q9HDM0	Q9HDM0 fillobasidie
16	27	100.0	33	3 Q9HDM9	Q9HDM9 fillobasidie
17	27	100.0	38	3 Q9VCH2	Q9VCH2 fillobasidie
18	27	100.0	48	5 Q9VCH2	Q9VCH2 drosophila
19	27	100.0	49	5 Q9NHP4	Q9NHP4 penaeus mon

20	27	100.0	51	10 Q9S993	Q9S993 brassica na
21	27	100.0	59	4 Q14846	Q14846 homo sapien
22	27	100.0	62	11 Q63326	Q63326 rattus norv
23	27	100.0	64	10 Q23989	Q23989 hordeum vul
24	27	100.0	72	14 Q75534	Q75534 human immun
25	27	100.0	72	14 Q75539	Q75539 human immun
26	27	100.0	74	10 Q41201	Q41201 nicotiana p
27	27	100.0	75	2 Q34601	Q34601 bacillus su
28	27	100.0	79	2 Q55785	Q55785 synechocyst
29	27	100.0	80	1 Q9V2U3	Q9V2U3 methanococc
30	27	100.0	82	6 Q97786	Q97786 bos taurus
31	27	100.0	83	4 Q9H4R6	Q9H4R6 homo sapien
32	27	100.0	85	2 Q44066	Q44066 aeromonas h
33	27	100.0	86	2 Q91270	Q91270 pseudomonas
34	27	100.0	87	2 Q9K483	Q9K483 streptomyce
35	27	100.0	87	10 Q40005	Q40005 hordeum vul
36	27	100.0	89	14 Q9YV39	Q9YV39 human immun
37	27	100.0	89	14 Q9YV38	Q9YV38 human immun
38	27	100.0	89	14 Q9YV37	Q9YV37 human immun
39	27	100.0	89	14 Q9YV36	Q9YV36 human immun
40	27	100.0	89	14 Q9YV35	Q9YV35 human immun
41	27	100.0	89	14 Q9YV34	Q9YV34 human immun
42	27	100.0	89	14 Q9YV33	Q9YV33 human immun
43	27	100.0	89	14 Q9YV32	Q9YV32 human immun
44	27	100.0	89	14 Q9YV31	Q9YV31 human immun
45	27	100.0	89	14 Q9W9P8	Q9W9P8 human immun

ALIGNMENTS

RESULT 1	ID	Q16350	PRELIMINARY:	PRT:	16 AA.
AC	Q16350	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)				
DT	01-NOV-1998 (TREMBLrel. 08, Last annotation update)				
DE	CRYSTATHIONINE BETA-SYNTHASE (FRAGMENT).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID:9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-95282779; PubMed-776255;				
RA	Sebastio G., Sperandeo M.P., Panico M., de Franchis R., Kraus J.P.,				
RA	Andria G.;				
RT	"The molecular basis of homocystinuria due to cystathionine beta-				
RT	synthase deficiency in Italian families, and report of four novel				
RT	mutations.";				
RL	Am. J. Hum. Genet. 56:1324-1333(1995).				
DR	EMBL; S78267; AAB34404.1; -;				
FT	NON_TER				
SQ	SEQUENCE	16 AA; 1538 MW; 07455C146B001686 CRC64;			
Query Match					
Best Local Similarity 100.0%; Score 27; DB 4; Length 16;					
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
OY	1 HPGG 4				
DB					
	6 HPGG 9				
RESULT 2					
ID	Q9UR51	PRELIMINARY:	PRT:	22 AA.	
AC	Q9UR51	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)				

DE NEOFORMANS ISOLATE CBS884 MF (MF) GENE, PARTIAL CDS (FRAGMENT).
GN MF.
OS Filobasidiella neoformans var. neoformans.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Tremellales;
OC Tremellaceae; Filobasidiella.
OX NCBI_TaxID=40410;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CBS884, AND CBS6989;
RX MEDLINE-99380307; PubMed-10449476;
RA Halliday C.L., But T., Krockenberger M., Malik R., Ellis D.H.,
Carter D.A.;
RT "Presence of alpha and a mating types in environmental and clinical
RT collections of Cryptococcus neoformans var. gatliff strains from
RT Australia.";
RL J. Clin. Microbiol. 37:2920-2926(1999).
DR EMBL; AF155341; AAF19019.1; -;
DR EMBL; AF155340; AAF19018.1; -;
FT NON_TER 1 1
FT SEQUENCE 22 AA; 2271 MW; 05D0BB7A059FB40F CRC64;
SQ

Query Match 100.0%; Score 27; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPGG 4
Db 18 HPGG 21

RESULT 3
O9UR41 PRELIMINARY; PRT; 22 AA.
AC O9UR41;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-MAY-2000 (TREMBLrel. 16, last annotation update)
DE BACILLISPORA ISOLATE CBS6956 MF (MF) GENE, PARTIAL CDS (FRAGMENT).
GN MF.
OS Filobasidiella neoformans var. bacillispora.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Tremellales;
OC Tremellaceae; Filobasidiella.
OX NCBI_TaxID=37769;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CBS6956, 1408, 571 146, BAL 21, AND CBS5757;
RX MEDLINE-99380307; PubMed-10449476;
RA Halliday C.L., But T., Krockenberger M., Malik R., Ellis D.H.,
Carter D.A.;
RT "Presence of alpha and a mating types in environmental and clinical
RT collections of Cryptococcus neoformans var. gatliff strains from
RT Australia.";
RL J. Clin. Microbiol. 37:2920-2926(1999).
DR EMBL; AF155339; AAF19017.1; -;
DR EMBL; AF155335; AAF19013.1; -;
DR EMBL; AF155336; AAF19014.1; -;
DR EMBL; AF155337; AAF19015.1; -;
DR EMBL; AF155338; AAF19016.1; -;
DR InterPro; IP000308; -;
DR ProDom; PD000600; -; 1.
FT NON_TER 1 1
FT SEQUENCE 22 AA; 2231 MW; 1EC9A72BA05E85BF CRC64;
SQ

Query Match 100.0%; Score 27; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPGG 4
Db 18 HPGG 21

Db 18 HPGG 21

RESULT 4
O9UC01 PRELIMINARY; PRT; 23 AA.
AC O9UC01;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, last annotation update)
DE Y-23-R-NH2-PREDICTED INSULIN-LIKE GROWTH FACTOR IB- (103-124) EI AMIDE
DE IBE1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92390398; PubMed-1325646;
RA Siegfried J.M., Kasprzyk P.G., Treston A.M., Mulshine J.L.,
Quinn K.A., Cutillo F.;
RT "A mitogenic peptide amide encoded within the E peptide domain of the
RT insulin-like growth factor IB prohormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:8107-8111(1992).
SQ SEQUENCE 23 AA; 2508 MW; 40A5F3F520E3F789 CRC64;

Query Match 100.0%; Score 27; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPGG 4
Db 7 HPGG 10

RESULT 5
O9TU40 PRELIMINARY; PRT; 27 AA.
AC O9TU40;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, last annotation update)
DE INTERPHOTORECEPTOR RETINOID BINDING PROTEIN (FRAGMENT).
GN IRBP.
OS Mammutus primigenius (Siberian woolly mammoth).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Proboscidea; Elephantidae; Mammutus.
OX NCBI_TaxID=37349;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20022977; PubMed-10555277;
RA Greenwood A.D., Capelli C., Possner G., Paabo S.;
RT "Nuclear DNA sequences from late Pleistocene megafauna.";
RL Mol. Biol. Evol. 16:1466-1473(1999).
DR EMBL; AF155042; AAF12753.1; -;
KM Receptor.
FT NON_TER 1 1
FT SEQUENCE 27 AA; 3052 MW; 167D5082BB341B42 CRC64;
SQ

Query Match 100.0%; Score 27; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPGG 4
Db 13 HPGG 16

RESULT 6
O9TU39

ID Q9TU39 PRELIMINARY; PRT; 27 AA.
AC Q9TU39;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE INTERHOMORECEPTOR RETINOID BINDING PROTEIN (FRAGMENT).
GN IRBP.
OS Elephas maximus (Indian elephant).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Proboscidea; Elephantidae; Elephas.
OX NCBI_TaxID=9783;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20022977; PubMed=10555277;
RA Greenwood A.D., Capelli C., Possner G., Paabo S.;
RT "Nuclear DNA sequences from late Pleistocene megafauna";
RL Mol. Biol. Evol. 16:1466-1473(1999).
DR EMBL; AF15043; AAF12754.1; -.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 27 27
SQ SEQUENCE 27 AA; 3052 MW; 167D5082B341B42 CRC64;

Query Match 100.0%; Score 27; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPGG 4
|
|
|
|
DB 13 HPGG 16

RESULT 7
O9HF31 PRELIMINARY; PRT; 33 AA.
ID O9HF31;
AC O9HF31;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PHEROMONE PRECURSOR MATA1PHA (FRAGMENT).
GN MAT-ALPHA.
OS Filobasidiella neoformans var. neoformans.
OC Eukaryota; Fungi; Basidiomycota; Hymenycetes; Tremellales;
OC Tremellaceae; Filobasidiella.
OX NCBI_TaxID=40410;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-UM-16;
RC MEDLINE=20251028; PubMed=10790143;
RA Chaturvedi S., Rodeghier B., Fan J., McClelland C.M., Wickes B.L.,
RT "Direct PCR of Cryptococcus neoformans MATA1PHA and MATA pHEROMONES to determine mating type, ploidy, and variety: a tool for epidemiological and molecular pathogenesis studies";
RL J. Clin. Microbiol. 38:2007-2009(2000).
DR EMBL; AF226905; AAG41294.1; -.
FT NON_TER 1 1
FT NON_TER 33 33
SQ SEQUENCE 33 AA; 3402 MW; 39002A095DF450A5 CRC64;

Query Match 100.0%; Score 27; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPGG 4
|
|
|
|
DB 25 HPGG 28

RESULT 8
O9HF29

ID O9HF29 PRELIMINARY; PRT; 33 AA.
AC O9HF29;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PHEROMONE PRECURSOR MATA1PHA (FRAGMENT).
GN MAT-ALPHA.
OS Filobasidiella neoformans var. neoformans.
OC Eukaryota; Fungi; Basidiomycota; Hymenycetes; Tremellales;
OC Tremellaceae; Filobasidiella.
OX NCBI_TaxID=40410;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-UM-276;
RC MEDLINE=20251028; PubMed=10790143;
RA Chaturvedi S., Rodeghier B., Fan J., McClelland C.M., Wickes B.L.,
RT "Direct PCR of Cryptococcus neoformans MATA1PHA and MATA pHEROMONES to determine mating type, ploidy, and variety: a tool for epidemiological and molecular pathogenesis studies";
RL J. Clin. Microbiol. 38:2007-2009(2000).
DR EMBL; AF226937; AAG41326.1; -.
FT NON_TER 1 1
FT NON_TER 33 33
SQ SEQUENCE 33 AA; 3430 MW; EE502A095DF450B7 CRC64;

Query Match 100.0%; Score 27; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPGG 4
|
|
|
|
DB 25 HPGG 28

RESULT 9
O9HF28 PRELIMINARY; PRT; 33 AA.
ID O9HF28;
AC O9HF28;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PHEROMONE PRECURSOR MATA1PHA (FRAGMENT).
GN MAT-ALPHA.
OS Cryptococcus neoformans (Filobasidiella neoformans).
OC Eukaryota; Fungi; Basidiomycota; Hymenycetes; Tremellales;
OC Tremellaceae; Filobasidiella.
OX NCBI_TaxID=5207;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-UM-2;
RC Chaturvedi S., Rodeghier B., Fan J., McClelland C.M., Wickes B.L.,
RT "Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases."
DR EMBL; AF226942; AAG41331.1; -.
FT NON_TER 1 1
FT NON_TER 33 33
SQ SEQUENCE 33 AA; 3430 MW; EE502A095DF450B7 CRC64;

Query Match 100.0%; Score 27; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPGG 4
|
|
|
|
DB 25 HPGG 28

RESULT 10
O9HF27 PRELIMINARY; PRT; 33 AA.

AC 09HF27;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE PHEROMONE PRECURSOR MATALPHA (FRAGMENT).
GN MAT-ALPHA.
OS Cryptococcus neoformans (Filobasidiella neoformans).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Tremellales;
OC Tremellaceae; Filobasidiella.
OX NCBI_TaxID=5207;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-UM-4;
RA Chaturvedi S.; Rodeghier B., Fan J., McClelland C.M., Wickes B.L.,
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF226944; AAC4133.1; -.
FT NON_TER 1 1
FT NON_TER 33 33
SQ SEQUENCE 33 AA; 3530 MW; 0781E70946ED4CE6 CRC64;

Query Match 100.0%; Score 27; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
ID 11111
DB 25 HPGG 28

RESULT 11
ID 09HF26 PRELIMINARY; PRT; 33 AA.
AC 09HF26;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE PHEROMONE PRECURSOR MATALPHA (FRAGMENT).
GN MAT-ALPHA.
OS Cryptococcus neoformans (Filobasidiella neoformans).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Tremellales;
OC Tremellaceae; Filobasidiella.
OX NCBI_TaxID=5207;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC32045;
RA Chaturvedi S.; Rodeghier B., Fan J., McClelland C.M., Wickes B.L.,
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF226946; AAC4133.1; -.
FT NON_TER 1 1
FT NON_TER 33 33
SQ SEQUENCE 33 AA; 3470 MW; 0795B64C46ED4CE6 CRC64;

Query Match 100.0%; Score 27; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
ID 11111
DB 25 HPGG 28

RESULT 12
ID 09HF25 PRELIMINARY; PRT; 33 AA.
AC 09HF25;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE PHEROMONE PRECURSOR MATALPHA (FRAGMENT).

GN MAT-ALPHA.
OS Cryptococcus neoformans (Filobasidiella neoformans).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Tremellales;
OC Tremellaceae; Filobasidiella.
OX NCBI_TaxID=5207;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NYS-169A;
RA Chaturvedi S.; Rodeghier B., Fan J., McClelland C.M., Wickes B.L.,
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF226948; AAC41337.1; -.
FT NON_TER 1 1
FT NON_TER 33 33
SQ SEQUENCE 33 AA; 3456 MW; 0792284C46ED4CE6 CRC64;

Query Match 100.0%; Score 27; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
ID 11111
DB 25 HPGG 28

RESULT 13
ID 09HDP1 PRELIMINARY; PRT; 33 AA.
AC 09HDP1;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE PHEROMONE PRECURSOR MATALPHA (MAT-ALPHA PHEROMONE) (FRAGMENT).
GN MAT-ALPHA.
OS Filobasidiella neoformans var. neoformans.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Tremellales;
OC Tremellaceae; Filobasidiella.
OX NCBI_TaxID=40410;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NYS-172;
RX MEDLINE-20251028; PubMed-10790143;
RA Chaturvedi S.; Rodeghier B., Fan J., McClelland C.M., Wickes B.L.,
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RT "Direct PCR of Cryptococcus neoformans MATalpha and MATra pheromones to determine mating type, ploidy, and variety: a tool for epidemiological and molecular pathogenesis studies."
RT J. Clin. Microbiol. 38:2007-2009(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-NYS1649; USC1789, USC1898, AND WM148;
RA Chaturvedi S.; Rodeghier B., Fan J., Wickes B., Chaturvedi V.;
RT "Cryptococcus neoformans MAT-alpha pheromone sequence."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF226889; AAC41278.1; -.
DR EMBL; AF214057; AAC41259.1; -.
DR EMBL; AF214059; AAC41261.1; -.
DR EMBL; AF214060; AAC41262.1; -.
DR EMBL; AF214064; AAC41266.1; -.
FT NON_TER 1 1
FT NON_TER 33 33
SQ SEQUENCE 33 AA; 3470 MW; 0795B64C46ED4CE6 CRC64;

Query Match 100.0%; Score 27; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
ID 11111
DB 25 HPGG 28


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RESULT 14
Q9HDP0 PRELIMINARY; PRT; 33 AA.
ID Q9HDP0;
AC Q9HDP0;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE PHEROMONE PRECURSOR MATALPHA (FRAGMENT).
GN MAT-ALPHA.
OS Cryptococcus neoformans var. grubii.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Tremellales;
OC Tremellaceae; Filobasidiella.
OX NCBI_TaxID=135857;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VARIOUS STRAINS;
RX MEDLINE=20251028; PubMed=10790143;
RA Chaturvedi S., Rodeghier B., Fan J., McClelland C.M., Wickes B.L.,
  Chaturvedi V.;
RT "Direct PCR of Cryptococcus neoformans MATalpha and MATa pheromones to
  determine mating type, ploidy, and variety: a tool for epidemiological
  RT and molecular pathogenesis studies.";
RL J. Clin. Microbiol. 38:2007-2009(2000).
DR EMBL; AF226888; AAG41277.1; -
DR EMBL; AF226880; AAG41269.1; -
DR EMBL; AF226881; AAG41270.1; -
DR EMBL; AF226882; AAG41272.1; -
DR EMBL; AF226883; AAG41273.1; -
DR EMBL; AF226884; AAG41274.1; -
DR EMBL; AF226885; AAG41275.1; -
DR EMBL; AF226886; AAG41276.1; -
DR EMBL; AF226887; AAG41276.1; -
FT NON_TER 1 1
FT NON_TER 33 33
SQ SEQUENCE 33 AA; 3470 MW; 0795B64C6EDACE6 CRC64;

Query Match 100.0%; Score 27; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
   ||||
Db 25 HPGG 28

RESULT 15
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ID Q9HDM0;
AC Q9HDM0;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE PHEROMONE PRECURSOR MATALPHA (MAT-ALPHA PHEROMONE) (FRAGMENT).
GN MAT-ALPHA.
OS Filobasidiella neoformans var. neoformans.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Tremellales;
OC Tremellaceae; Filobasidiella.
OX NCBI_TaxID=40410;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VARIOUS STRAINS;
RX MEDLINE=20251028; PubMed=10790143;
RA Chaturvedi S., Rodeghier B., Fan J., McClelland C.M., Wickes B.L.,
  Chaturvedi V.;
RT "Direct PCR of Cryptococcus neoformans MATalpha and MATa pheromones to
  determine mating type, ploidy, and variety: a tool for epidemiological
  RT and molecular pathogenesis studies.";
RL J. Clin. Microbiol. 38:2007-2009(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC28957, UM3, AND UM8;

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RA Chaturvedi S., Rodeghier B., Fan J., Wickes B., Chaturvedi V.;
RT "Cryptococcus neoformans MAT-alpha pheromone sequence.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF226913; AAG41302.1; -
DR EMBL; AF214054; AAG41256.1; -
DR EMBL; AF214062; AAG41264.1; -
DR EMBL; AF214063; AAG41265.1; -
DR EMBL; AF226891; AAG41280.1; -
DR EMBL; AF226892; AAG41281.1; -
DR EMBL; AF226895; AAG41284.1; -
DR EMBL; AF226896; AAG41285.1; -
DR EMBL; AF226897; AAG41286.1; -
DR EMBL; AF226898; AAG41287.1; -
DR EMBL; AF226899; AAG41288.1; -
DR EMBL; AF226900; AAG41289.1; -
DR EMBL; AF226901; AAG41290.1; -
DR EMBL; AF226902; AAG41291.1; -
DR EMBL; AF226906; AAG41295.1; -
DR EMBL; AF226907; AAG41296.1; -
DR EMBL; AF226908; AAG41297.1; -
DR EMBL; AF226910; AAG41299.1; -
DR EMBL; AF226911; AAG41300.1; -
DR EMBL; AF226912; AAG41301.1; -
FT NON_TER 1 1
FT NON_TER 33 33
SQ SEQUENCE 33 AA; 3432 MW; 39002A0946F5E0A5 CRC64;

Query Match 100.0%; Score 27; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPGG 4
   ||||
Db 25 HPGG 28

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Search completed: August 9, 2001, 20:36:15
Job time: 714 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 9, 2001, 20:24:16 ; Search time 79.24 Seconds
(without alignments)
9.946 Million cell updates/sec

Title: US-09-367-013b-2_COPY_390_402
Perfect score: 76
Sequence: 1 GGLNYQIEHHLFP 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_0601:*
1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT:*
2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT:*
3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT:*
4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT:*
5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT:*
6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT:*
7: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT:*
8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT:*
9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT:*
10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT:*
11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT:*
12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT:*
13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT:*
14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT:*
15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT:*
16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT:*
17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT:*
18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT:*
19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT:*
20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT:*
21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT:*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	100.0	87	19	AAW84144
2	76	100.0	355	19	AAW84139
3	76	100.0	443	20	AAV17751
4	76	100.0	447	20	AAV21891
5	76	100.0	447	21	AAV96721
6	76	100.0	454	21	AAV51355
7	76	100.0	457	19	AAW84137
8	76	100.0	457	20	AAW85504
9	76	100.0	457	20	AAW85121
10	76	100.0	457	21	AAV92599
11	76	100.0	457	21	AAV56045

12	76	100.0	457	22	AAW31684
13	76	100.0	473	21	AAV51353
14	71	93.4	422	21	AAV96722
15	67	88.2	448	21	AAV71551
16	67	88.2	520	22	AAW46440
17	67	88.2	525	21	AAV51354
18	67	88.2	525	22	AAW46810
19	66	86.8	87	21	AAW83240
20	66	86.8	446	20	AAW85122
21	66	86.8	448	17	AAW98455
22	66	86.8	448	19	AAW67471
23	66	86.8	448	20	AAW98130
24	66	86.8	448	21	AAV51349
25	66	86.8	462	21	AAV71552
26	65	85.5	469	21	AAV71555
27	64	84.2	54	21	AAW83245
28	64	84.2	54	21	AAW83246
29	64	84.2	85	21	AAW83233
30	64	84.2	85	21	AAW83234
31	64	84.2	87	21	AAW83239
32	64	84.2	131	19	AAW84143
33	64	84.2	143	19	AAW84145
34	64	84.2	211	19	AAW84151
35	64	84.2	211	20	AAW85130
36	64	84.2	218	20	AAW95509
37	64	84.2	218	21	AAW84698
38	64	84.2	218	21	AAV92613
39	64	84.2	224	21	AAV51350
40	64	84.2	284	21	AAV51351
41	64	84.2	286	21	AAW85842
42	64	84.2	287	21	AAV95447
43	64	84.2	294	21	AAV95448
44	64	84.2	326	21	AAW29291
45	64	84.2	326	21	AAW53863

ALIGNMENTS

RESULT 1	
AAW84144	
ID AAW84144 standard; Peptide: 87 AA.	
XX	
AC AAW84144;	
XX	
DT 15-FEB-1999 (first entry)	
XX	
DE Desaturase enzyme peptide sequence.	
XX	
KW Fatty acid; desaturase; polyunsaturated fatty acid;	
KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;	
KW cancer; diabetes; eczema; platelet aggregation; vasodilation;	
KW cholesterol level; endometriosis; premenstrual syndrome;	
KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;	
KW acute respiratory syndrome; hypertension; inflammatory skin disorder.	
XX	
OS Unidentified.	
XX	
FN W09846763-A1.	
PD	
PD 22-OCT-1998.	
XX	
PF 10-APR-1998; 98WO-US07126.	
XX	
PR 11-APR-1997; 97US-0834655.	
XX	
PA (ABBO) ABBOTT LAB.	
XX (CALJ) CALGENE LLC.	
PI Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P;	
XX Thurmond J;	
DR WPI: 1998-594582/50.	

Amino acid sequenc
Protein bcoe with
E. gracilis fatty
Florida bitterbush
C. purpureus delta
Protein b5pp with
P. patens delta-6-d
Delta 6 desaturase
Borage delta-6-des
Borage delta-6-des
Sunflower HADES pr
Corn sphingolipid
Wheat sphingolipid
CyB5RP fatty acid
Delta 6 desaturase
CyB5RP fatty acid
Sunflower hypothe
CyB5RP fatty acid
Desaturase enzyme
Desaturase enzyme
Human desaturase e
A desaturase enzym
Amino acid sequenc
Amino acid sequenc
Human desaturase h
Protein d5ipu with
Protein b5ipu with
Breast and ovarian
Putative human des
Human delta-5-des
Arabidopsis thalia
Arabidopsis thalia

XX New isolated fatty acid desaturase enzymes - used for the production
PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical
PT compositions, nutritional compositions, cosmetics or animal feed
XX
XX

PS Example 2; Pages 105-106; 165pp; English.

CC The present sequence represents a peptide derived from a desaturase
CC enzyme. The specification describes methods for desaturating a
CC fatty acid and for producing a desaturated fatty acid by expressing
CC increased levels of a desaturase. Desaturases can be used for
CC desaturating fatty acids. The enzymes can be used to produce
CC polyunsaturated fatty acids, which can be used for treating malnutrition,
CC in pharmaceutical compositions, in cosmetics or in animal feed. The
CC polyunsaturated fatty acids can be used for treating e.g. restenosis
CC after angioplasty, inflammation, rheumatoid arthritis, asthma, psoriasis,
CC cancer, diabetes or eczema or reduce blood pressure. They can also be
CC used to inhibit platelet aggregation, cause vasodilation, lower
CC cholesterol levels, inhibit proliferation of vessel wall smooth muscle
CC and fibrous tissue, reduce or prevent gastro-intestinal bleeding and
CC other side effects caused by non-steroidal anti-inflammatory drugs,
CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic
CC encephalomyelitis and chronic fatigue after viral infections, treat AIDS,
CC multiple sclerosis, acute respiratory syndrome, hypertension and
CC inflammatory skin disorders.

SO Sequence 87 AA:

Query Match 100.0%; Score 76; DB 19; Length 87;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGLNYQIEHHLP 13
|||
DB 22 gglnyqiehhlp 34

RESULT 2
AAW84139
ID AAW84139 standard; Peptide: 355 AA.

XX AAW84139;

DT 15-FEB-1999 (first entry)

DE Desaturase enzyme peptide sequence.

XX Fatty acid; desaturase; polyunsaturated fatty acid;
KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
KW cholesterol level; endometriosis; premenstrual syndrome;
KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
KW acute respiratory syndrome; hypertension; inflammatory skin disorder.

XX Unidentified.

XX WO9846763-A1.

PD 22-OCT-1998.

PF 10-APR-1998; 98WO-US07126.

PR 11-APR-1997; 97US-0834655.

PA (ABBO) ABBOTT LAB.
PA (CALJ) CALGENE LLC.

PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P;
PI Thurmond J;

DR WPI; 1998-594582/50.

PT New isolated fatty acid desaturase enzymes - used for the production
PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical
PT compositions, nutritional compositions, cosmetics or animal feed
XX
XX

PS Example 2; Pages 101-102; 165pp; English.

CC The present sequence represents a peptide derived from a desaturase
CC enzyme. The specification describes methods for desaturating a
CC fatty acid and for producing a desaturated fatty acid by expressing
CC increased levels of a desaturase. Desaturases can be used for
CC desaturating fatty acids. The enzymes can be used to produce
CC polyunsaturated fatty acids, which can be used for treating malnutrition,
CC in pharmaceutical compositions, in cosmetics or in animal feed. The
CC polyunsaturated fatty acids can be used for treating e.g. restenosis
CC after angioplasty, inflammation, rheumatoid arthritis, asthma, psoriasis,
CC cancer, diabetes or eczema or reduce blood pressure. They can also be
CC used to inhibit platelet aggregation, cause vasodilation, lower
CC cholesterol levels, inhibit proliferation of vessel wall smooth muscle
CC and fibrous tissue, reduce or prevent gastro-intestinal bleeding and
CC other side effects caused by non-steroidal anti-inflammatory drugs,
CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic
CC encephalomyelitis and chronic fatigue after viral infections, treat AIDS,
CC multiple sclerosis, acute respiratory syndrome, hypertension and
CC inflammatory skin disorders.

SO Sequence 355 AA:

Query Match 100.0%; Score 76; DB 19; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGLNYQIEHHLP 13
|||
DB 288 gglnyqiehhlp 300

RESULT 3
AAV17751
ID AAV17751 standard; Protein: 443 AA.

XX AAV17751;

DT 11-AUG-1999 (first entry)

DE Caenorhabditis elegans Delta 6 desaturase Cgd6.1.

XX Caenorhabditis elegans; C. elegans; Delta 6 desaturase; Cgd6.1;
KW gamma-linolenic acid; GFA; plant fatty acid; octadecetraenoic acid;
KW OTA; eicosanoid; eczema; mastalgia; atherosclerosis; coronary disease;
KW hypercholesterolemia; diabetic neuropathy; viral infection; acne;
KW hypertension; cirrhosis; cancer.

XX Caenorhabditis elegans.

XX WO9927111-A1.

PN 03-JUN-1999.

PF 24-NOV-1998; 98WO-GB03507.

PR 24-NOV-1997; 97GB-0024783.

PA (UYBR-) UNIV BRISTOL.

PI Napier JA;

DR WPI; 1999-370905/31.

DR N-PSDB; AAX76589.

PT Desaturase enzymes, the genes encoding them and their uses
XX
XX
XX Claim 1; Fig 1; 44pp; English.

XX The present sequence is *Caenorhabditis elegans* Delta 6 desaturase,
CC designated Cede.1. Desaturase enzymes (I) may be used as immunogens to
CC raise and select antibodies (which may be used in immunoassays, and
CC diagnostic tests to detect the presence of (I) in a sample, or to purify
CC (I) or as a selectable marker for transformation, especially
CC transformations involving plants. (I) can be used to produce gamma-
CC linolenic acid (GLA) (and derivatives of it), which is a high value
CC plant fatty acid that is widely used in medicine for the preparation of
CC compositions for treating disorders associated with deficiencies in GLA
CC or deficiencies in metabolites derived in vivo from GLA, such as
CC octadecetraenoic acid (OTA) and eicosanoids. Disorders that may be
CC treated with GLA and OTA include eczema, mastalgia, atherosclerosis,
CC hypercholesterolaemia, coronary disease, diabetic neuropathy, viral
CC infections, acne, hypertension, cirrhosis and cancer. The nucleotide
CC sequences (II) encoding (I) may be used as probes or primers. Probes may
CC be used to identify and purify nucleic acids and so may be used in
CC diagnosis to detect the presence of (II) in a sample. Primers are useful
CC for amplifying DNA by polymerase chain reaction (PCR). (II) may also be
CC used to prepare an organism that is either chill resistant or that
CC accumulates GLA or metabolites derived from GLA. Hybridizing DNA
CC molecules may be used as anti-sense molecules to alter the expression of
CC (II) by binding to it and preventing transcription. Hybridizing
CC molecules may also be provided as ribozymes which regulate expression by
CC cleaving RNA molecules.

XX
SQ Sequence 443 AA;

Query Match 100.0%; Score 76; DB 20; Length 443;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGLNYQIEHHLP 13
| | | | | | | | | | | | | | | | | |
DB 378 gglnyqiehhlp 390

RESULT 4

ID AAY21891 standard; Protein; 447 AA.

XX AAY21891;

XX 24-SEP-1999 (first entry)

DE C. elegans delta 5-fatty acid desaturase.

XX Delta 5-fatty acid desaturase; dihomogamma linolenic acid; gene therapy;
KW arachidonic acid; cholesterol; polyunsaturated fatty acid; foodstuff;
XX dietary supplement; prostaglandin.

OS *Caenorhabditis elegans*.

XX WO933958-A2.

XX 08-JUL-1999.

XX 23-DEC-1998; 98WO-GB03895.

XX 29-JUN-1998; 98GB-0014034.

XX 23-DEC-1997; 97GB-0027256.

XX (UyBR-) UNIV BRISTOL.

XX Michaelson L, Napier JA, Stobart K;

XX WPI; 1999-444067/37.

XX N-PSDB; AAX86961.

XX New isolated delta5-fatty acid desaturase enzymes useful in gene
PT therapy
XX

PS Claim 18; Page 23; 36pp; English.

XX The invention provides delta 5-fatty acid desaturases obtained from
CC *Moriterella alpina* and *Caenorhabditis elegans*. The Delta 5-fatty acid
CC desaturases catalyze the production of polyunsaturated fatty acids, e.g.
CC the conversion of dihomogamma linolenic acid to arachidonic acid. The
CC genes can be used in gene therapy as a preventative treatment, e.g. in
CC patients suffering from high levels of cholesterol or other conditions
CC where administration of polyunsaturated fatty acids may have beneficial
CC disease-preventative effects. The polyunsaturated fatty acids can be used
CC in foodstuffs or dietary supplements. The Delta 5-fatty acid desaturases
CC can also be used for the synthesis of prostaglandins or modulation of the
CC synthesis. The products can also be used for detection and diagnosis. The
CC present sequence represents the C. elegans delta 5-fatty acid desaturase.

XX
SQ Sequence 447 AA;

Query Match 100.0%; Score 76; DB 20; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGLNYQIEHHLP 13
| | | | | | | | | | | | | | | | | |
DB 379 gglnyqiehhlp 391

RESULT 5

ID AAY96721 standard; Protein; 447 AA.

XX AAY96721;

XX 26-SEP-2000 (first entry)

DE C. elegans fatty acid delta-5-desaturase.

XX Fatty acid delta-5 desaturase; polyunsaturated; oil; seed;
KW infant formula; dietary supplement.

OS *Caenorhabditis elegans*.

XX WO200034439-A1.

XX 15-JUN-2000.

XX 06-DEC-1999; 99WO-US28655.

XX 07-DEC-1998; 98US-0111301.

XX (UNIW) UNIV WASHINGTON STATE RES FOUND.

XX Browse JA, Wallis JG, Watts JL;

XX WPI; 2000-431293/37.

XX N-PSDB; AAY51232.

XX Purified protein having desaturase activity, useful for creating a
PT double-bond between two carbons
PT

XX Claim 3; Fig 6A; 74pp; English.

XX This is the *Caenorhabditis elegans* fatty acid delta-5 desaturase. The
CC cDNA sequence is useful for recombinant production of the enzyme and for
CC generating transformed host cells and transgenic plants. The desaturase
CC can be used for creating a double-bond between two carbons. In
CC particular, the enzyme is useful for producing polyunsaturated fatty
CC acids and for generating enzyme-specific antibodies useful for
CC identifying desaturases. Oil-seed plants may be engineered to incorporate
CC the enzyme, so that the plants produce seed oil rich in fatty acids. The
CC fatty acids could be incorporated usefully into infant formula, foods of
CC all kinds, dietary supplements, nutraceutical and pharmaceutical
CC formulations.

XX Sequence 447 AA:
SQ

Query Match 100.0%; Score 76; DB 21; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGLNVOIEHHLP 13
DB 379 gglinyqiehhlp 391

RESULT 6
AAV51355
ID AAV51355 standard; Protein; 454 AA.

AC AAV51355;

DT 27-APR-2000 (first entry)

DE Protein 25bce with delta6 fatty acid desaturase activity.

KW sphingolipid desaturase; sldl; sphingobase; ceramide; capnoid;
KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;
KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;
KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
KW pharmaceutical; food; chemical raw material.

OS Unidentified.

PN DE19828850-A1.

PD 30-DEC-1999.

PF 27-JUN-1998; 98DE-1028850.

PR 27-JUN-1998; 98DE-1028850.

PA (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.

PI Heinz E. Zaehring U, Schmidt H, Sperling P;

DR WPI; 2000-127549/12.

PT New sphingolipid desaturase that selectively introduces double bond
into sphingolipids and capnoids -

PS Disclosure; Fig 16; 62pp; German.

XX This invention describes a novel sphingolipid desaturase that selectively
CC introduces a double bond into the sphingobase of the ceramide residue of
CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
CC desaturase, or a vector containing the DNA sequence, can be used to
CC produce transgenic plants, especially crop plants, with an increased or
CC decreased delta-8-unsaturated long-chain base content or an altered
CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
CC compensate for a delta-8-unsaturated long-chain base deficiency, to
CC exclude production of delta-8-unsaturated bases, to increase tolerance
CC or resistance to soil salinity, ion stress or toxicity, drought, wet
CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
CC alter size growth and flowering time. Cells, transgenic organisms or
CC plants containing the DNA sequence can be used to produce sphingolipids
CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
CC materials. This sequence represents a protein which has delta6 fatty acid
CC desaturase activity which is described in the method of the invention.

SQ Sequence 454 AA:

Query Match 100.0%; Score 76; DB 21; Length 454;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGLNVOIEHHLP 13
DB 386 gglinyqiehhlp 398

RESULT 7
AAM84137
ID AAM84137 standard; Protein; 457 AA.

AC AAM84137;

DT 15-FEB-1999 (first entry)

DE A delta-6 desaturase enzyme.

KW Fatty acid; delta-6 desaturase; polyunsaturated fatty acid;
KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
KW cholesterol level; endometriosis; premenstrual syndrome;
KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
KW acute respiratory syndrome; hypertension; inflammatory skin disorder.

OS Mortierella alpina.

PN WO9846763-A1.

PD 22-OCT-1998.

PF 10-APR-1998; 98WO-US07126.

PR 11-APR-1997; 97US-0834655.

PA (ABBO) ABBOTT LAB.
(CALJ) CALGENE LLC.

PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P;

DR WPI; 1998-594582/50.

DR N-PSDB; AAV63624.

PT New isolated fatty acid desaturase enzymes - used for the production
of polyunsaturated fatty acids for use in, e.g., pharmaceutical
compositions, nutritional compositions, cosmetics or animal feed
XX
XX
XX Claim 3; Fig 3A-E; 165pp; English.

XX The present sequence represents a Mortierella alpina fatty acid delta-6
CC desaturase enzyme. The enzyme sequence is used in the methods of
CC the invention. The specification describes methods for desaturating a
CC fatty acid and for producing a desaturated fatty acid by expressing
CC increased levels of a desaturase. The present desaturase is an enzyme
CC which introduces a double bond carbons 6 and 7 from the carboxyl end of
CC a fatty acid molecule. The enzyme can be used for desaturating fatty
CC acids. The enzyme can be used to produce polyunsaturated fatty acids,
CC which can be used for treating malnutrition, in pharmaceutical
CC compositions, in cosmetics or in animal feed. The polyunsaturated fatty
CC acids can be used for treating e.g. restenosis after angioplasty,
CC inflammation, rheumatoid arthritis, asthma, psoriasis, cancer, diabetes
CC or eczema or reduce blood pressure. They can also be used to inhibit
CC platelet aggregation, cause vasodilation, lower cholesterol levels,
CC inhibit proliferation of vessel wall smooth muscle and fibrous tissue,
CC reduce or prevent gastro-intestinal bleeding and other side effects
CC caused by non-steroidal anti-inflammatory drugs, prevent or treat
CC endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis
CC and chronic fatigue after viral infections, treat AIDS, multiple
CC sclerosis, acute respiratory syndrome, hypertension and inflammatory skin
CC disorders.

SQ Sequence 457 AA:

Query Match 100.0%; Score 76; DB 19; Length 457;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGLNYQIEHHLP 13
DB 390 gglnyqiehhlp 402

RESULT 8
ID AAM95504 standard; peptide: 457 AA.
XX
AC AAM95504;
XX
DT 26-MAR-1999 (first entry)
XX
DE Mortierella alpina delta 6 desaturase.
XX
KM Delta 6 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil;
KM polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;
KM stearidonic acid; eicosapentaenoic acid; maintenance; feeding formula;
KM dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;
KM rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;
KM diabetes; cosmetic; animal feed.
XX
OS Mortierella alpina.
XX
PN MO9846764-A1.
XX
PD 22-OCT-1998.
XX
PF 10-APR-1998; 98MO-US07421.
XX
PR 24-OCT-1997; 97US-0956985.
PR 11-APR-1997; 97US-0833610.
PR 11-APR-1997; 97US-0834033.
PR 11-APR-1997; 97US-0834655.
XX
PA (ABBO) ABBOTT LAB.
PA (CALJ) CALGENE LLC.
XX
PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P;
PI Thurmond J;
XX
DR WPI: 1999-080739/07.
DR N-PSDB; AAX00889.
XX
PT Nucleic acid construct able to express fatty acid desaturase in
PT plants - useful in human or animal nutrition, as cosmetics and
PT therapeutically, e.g. for restenosis, cancer and diabetes
XX
PS Claim 7; Fig 3A-E: 210pp; English.
XX
CC This represents a Mortierella alpina delta 6 desaturase. The invention
CC relates to a nucleic acid construct that contains at least one of the
CC nucleotide sequences (AAX00889 to AAX00891) encoding M. alpina delta 6,
CC delta 12 and delta 5 desaturases (AAM95504 to AAM95506) respectively,
CC coupled to an expression control sequence functional in plants.
CC Recombinant plant cells containing at least one DNA encoding a M. alpina
CC fatty acid desaturase (FAD), can be used for the production of
CC polyunsaturated fatty acid (PUFA). These recombinant cells or plants
CC containing them are used to produce oils such as linoleic acid,
CC arachidonic acid, gamma-linolenic acid, dihomo-gamma-linolenic acid,
CC stearidonic acid and eicosapentaenoic acid (EPA). These plant oils are
CC used: (i) to treat malnutrition; (ii) in infant feeding formulas, or
CC dietary supplements or substitutes, for use in humans or animals; (iii)
CC for treating disorders associated with inadequate consumption or
CC production of PUFA (or their metabolites such as prostaglandins), e.g.
CC restenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis,
CC psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics, and
CC (v) as animal feeds. Fragments of the DNA are used as probes to isolate

CC related coding sequences. Recombinant plants can produce high yields of
CC PUFA, since new pathways can be created and unwanted ones suppressed.
CC Plants can be engineered to express oils of particular PUFA composition,
CC e.g. one similar to that in human milk, and product recovery is simpler
CC than with e.g. fish.
XX
SQ Sequence 457 AA;

Query Match 100.0%; Score 76; DB 20; Length 457;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGLNYQIEHHLP 13
DB 390 gglnyqiehhlp 402

RESULT 9
ID AAM85121 standard; Protein: 457 AA.
XX
AC AAM85121;
XX
DT 11-FEB-1999 (first entry)
XX
DE A delta-6 desaturase enzyme amino acid sequence.
XX
KM Fatty acid; delta-6 desaturase; polyunsaturated fatty acid;
KM malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
KM cancer; diabetes; eczema; platelet aggregation; vasodilation;
KM cholesterol level; endometriosis; premenstrual syndrome;
KM myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
KM acute respiratory syndrome; hypertension; inflammatory skin disorder.
XX
OS Unidentified.
XX
PN MO9846765-A1.
XX
PD 22-OCT-1998.
XX
PF 10-APR-1998; 98MO-US07422.
XX
PR 11-APR-1997; 97US-0833610.
XX
PA (ABBO) ABBOTT LAB.
PA (CALJ) CALGENE LLC.
XX
PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P;
PI Thurmond J;
XX
DR WPI: 1999-009334/01.
XX
PT New nucleic acid encoding deltas and other desaturase enzymes -
PT useful in production of oils of increased arachidonic acid content,
PT used, e.g. for treating cancer, as foods, animal feeds and cosmetics
XX
PS Disclosure: Pages 95-96; 153pp; English.
XX
CC The present sequence represents a fatty acid delta-6 desaturase enzyme.
CC The specification describes methods for desaturating a fatty acid and
CC for producing a desaturated fatty acid by expressing increased levels of
CC a desaturase. The present desaturase is an enzyme which introduces a
CC double bond carbons 6 and 7 from the carboxyl end of a fatty acid
CC molecule. The enzyme can be used for desaturating fatty acids. The
CC enzyme can be used to produce polyunsaturated fatty acids, which can
CC be used for treating malnutrition, in pharmaceutical compositions,
CC in cosmetics or in animal feed. The polyunsaturated fatty acids can
CC be used for treating e.g. restenosis after angioplasty, inflammation,
CC rheumatoid arthritis, asthma, psoriasis, cancer, diabetes or eczema
CC or reduce blood pressure. They can also be used to inhibit platelet
CC aggregation, cause vasodilation, lower cholesterol levels, inhibit
CC proliferation of vessel wall smooth muscle and fibrous tissue.

CC The fatty acid desaturases are able to catalyse the conversion of oleic
CC acid to linoleic acid, linoleic acid to gamma-linolenic acid or of
CC alpha-linolenic acid to stearidonic acid. Transgenic insect cells

CC The invention relates to a method of generating novel compositions
CC comprising animal cells producing essential fatty acids (FAs). The animal
CC cells are produced by transforming cells, e.g. embryonic stem cells, with
CC nucleic acid encoding heterologous enzymes involved in fatty acid,
CC e.g. long chain or polyunsaturated fatty acid (PUFA) biosynthesis. This
CC sequence corresponds to a fungal delta6-desaturase whose coding sequence
CC is an example of a nucleic acid sequence used to transform the cells. The
CC essential FAs obtained can be used in nutritional formulations or animal
CC feed formulations. The long chain PUFAs can be used in nutritional
CC formulations, cosmetic formulations or animal feed formulations. The

CC products can also be used for producing transgenic animals which can be
CC used for producing essential FAs which can be used for producing
CC downstream products such as leukotrienes, thromboxanes, arachidonic acid,
CC eicosapentaenoic acid or docosahexaenoic acid. The products can also be
CC used in cell culture. The animal or milk fat produced can be administered
CC to treat malnutrition.

XX Sequence 457 AA;

Query Match 100.0%; Score 76; DB 21; Length 457;

Best Local Similarity 100.0%; Pred. No. 2.2e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 13; Conservative 0; Indels 0; Gaps 0;
OY 1 GGLNVOIEHHLP 13
|||||
DB 390 gglngqiehhlp 402

RESULT 12

AAB31684 ID AAB31684 standard; Protein: 457 AA.

XX AAB31684;

XX 30-APR-2001 (first entry)

DE Amino acid sequence of a fungal delta6 desaturase.

XX delta6 desaturase; desaturase gene; elongase gene; fatty acid;

KW eicosanoid; nutrition; infant formula; dietary supplement;

KM dietary substitute; animal feed.

OS Mortierella alpina.

XX MO200104636-A1.

XX 18-JAN-2001.

XX 11-JUL-2000; 2000MO-US19011.

XX 12-JUL-1999; 99US-0351525.

XX (UYOH-) UNIV OHIO.

XX Kopechick JJ, Kelder B;

DR WPI; 2001-182622/18.

DR N-PSDB; AAF25234.

XX New compositions comprising cells that express desaturases and

PT elongases, for synthesizing essential fatty acids or long-chain

PT polyunsaturated fatty acids, used in nutritional, cosmetic or animal

PT feed formulations

XX Disclosure; Fig 9; 93pp; English.

XX The present sequence represents a delta6 desaturase. The desaturase

CC polynucleotide sequence was used to transfect mammalian cells, to

CC produce animal cells expressing a desaturase gene and/or an elongase

CC gene. Compositions comprising cells of the invention are useful for

CC synthesizing essential fatty acids, their derivatives or downstream

CC products, as well as altered levels of long-chain polyunsaturated

CC fatty acids and eicosanoids. The compositions are useful in nutritional

CC formulae, e.g. infant formula, dietary supplements or dietary

CC substitutes for both humans and animals. The compositions are also

CC useful in cosmetic or animal feed formulations. Furthermore, the

CC compositions may also be used as fat free media or as research reagents.

XX Sequence 457 AA;

Query Match 100.0%; Score 76; DB 22; Length 457;

Best Local Similarity 100.0%; Pred. No. 2.2e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 13; Conservative 0; Indels 0; Gaps 0;
OY 1 GGLNVOIEHHLP 13
|||||
DB 390 gglngqiehhlp 402

RESULT 13

AAY51353 ID AAY51353 standard; Protein: 473 AA.

XX AAY51353;

XX 27-APR-2000 (first entry)

DE Protein b5cae with delta6 fatty acid desaturase activity.

XX Sphingolipid desaturase; sld; sphingobase; ceramide; capnoid;

KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;

KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;

KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;

KW pharmaceutical; food; chemical raw material.

XX Unidentified.

XX DE19828850-A1.

XX 30-DEC-1999.

XX 27-JUN-1998; 98DE-1028850.

XX 27-JUN-1998; 98DE-1028850.

XX (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.

XX Heinz E, Zaehring U, Schmidt H, Sperling P;

XX WPI; 2000-127549/12.

XX New sphingolipid desaturase that selectively introduces double bond

PT into sphingolipids and capnoids

PT Disclosure; Page 38-39; 62pp; German.

XX This invention describes a novel sphingolipid desaturase that selectively

CC introduces a double bond into the sphingobase of the ceramide residue or

CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid

CC desaturase, or a vector containing the DNA sequence, can be used to

CC produce transgenic plants, especially crop plants, with an increased or

CC decreased delta-8-unsaturated long-chain base content or an altered

CC delta-8-unsaturated long-chain base cis/trans ratio, especially to

CC compensate for a delta-8-unsaturated long-chain base deficiency, to

CC exclude production of delta-8-unsaturated bases, to increase tolerance

CC or resistance to soil salinity, ion stress or toxicity, drought, wet

CC conditions, cold or frost and/or phytopathogenic microorganisms, or to

CC alter size growth and flowering time. Cells, transgenic organisms or

CC plants containing the DNA sequence can be used to produce sphingolipids

CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids

CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw

CC materials. This sequence represents a protein which has delta6 fatty acid

CC desaturase activity which is described in the method of the invention.

XX Sequence 473 AA;

Query Match 100.0%; Score 76; DB 21; Length 473;

Best Local Similarity 100.0%; Pred. No. 2.3e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 13; Conservative 0; Indels 0; Gaps 0;
OY 1 GGLNVOIEHHLP 13
|||||
DB 408 gglngqiehhlp 420

XX	RESULT 14
AC	AAY96722
ID	AAY96722 standard; Protein: 422 AA.
XX	
DT	AAY96722;
XX	
XX	26-SEP-2000 (first entry)
DE	E. gracilis fatty acid delta-8 desaturase.
XX	
KW	Fatty acid delta-8 desaturase; polyunsaturated; oil; seed;
RW	infant formula; dietary supplement.
XX	
OS	Euglena gracilis.
XX	
FT	Key Location/Qualifiers
FT	Misc-difference 20..23
FT	/note= "encoded by GTC"
FT	Misc-difference 146..150
FT	/label= His-box_motif
FT	Misc-difference 183..187
FT	/label= His-box_motif
FT	Misc-difference 358..362
FT	/label= Variant_His-box_motif
XX	
PN	WO200034439-A1.
PD	15-JUN-2000.
XX	
PF	06-DEC-1999; 99WO-US28655.
PR	07-DEC-1998; 98US-O111301.
PA	(UNIW) UNIV WASHINGTON STATE RES FOUND.
PI	Browse JA, Wallis JG, Watts JL:
DR	WPI, 2000-431293/37.
N-PSDB;	AAAS1233.
Purified protein having desaturase activity, useful for creating a double-bond between two carbons	
Claim 1; Fig 7A; 74pp; English.	
This is the Euglena gracilis fatty acid delta-8 desaturase. The cDNA sequence is useful for recombinant production of the enzyme and for generating transformed host cells and transgenic plants. The desaturase can be used for creating a double-bond between two carbons. In particular, the enzyme is useful for producing polyunsaturated fatty acids and for generating enzyme-specific antibodies useful for identifying desaturases. Oil-seed plants may be engineered to incorporate the enzyme, so that the plants produce seed oil rich in fatty acids. The fatty acids could be incorporated usefully into infant formula, foods of all kinds, dietary supplements, nutraceutical and pharmaceutical formulations.	
Sequence 422 AA;	

ID	AA71551 standard; Protein; 448 AA.
AC	AA71551;
XX	
DT	12-OCT-2000 (first entry)
XX	
DE	Florida bitterbush delta-6 fatty acid desaturase.
XX	
KW	Florida bitterbush; delta-6 fatty acid desaturase; tartaric acid;
KW	transgenic plant; fatty acid; membrane-bound desaturase.
XX	
OS	Pteranmia pentandra.
XX	
PN	WO200032790-A2.
XX	
PD	08-JUN-2000.
XX	
PF	02-DEC-1999; 99MO-US28589.
XX	
PR	03-DEC-1998; 98US-0110784.
XX	
PA	(DUPO) DU PONT DE NEMOURS & CO E. I.
PI	
DR	Caboon EB, Caboon RE, Hiltz WD, Kinney AJ;
XX	
DR	WPI: 2000-412336/35.
XX	
DR	N-PSDB; AAD01349.
XX	
PT	Polynucleotide encoding delta-6 desaturase enzyme useful for producing
PT	transgenic plants and for producing antibodies specific to which is
PT	useful for screening cDNA expression libraries
XX	
PS	Claim 10; Page 40-41; 57pp; English.
XX	
CC	The present sequence is a delta-6 fatty acid desaturase protein sequence
CC	from clone pps.pK0011.ds.fis isolated from Florida bitterbush developing
CC	seed cDNA library. pps. The delta-6 desaturase enzyme catalyses the
CC	formation of tartaric acid, a fatty acid that has a triple bond at the
CC	delta-6 carbon. The present sequence is useful for producing
CC	transgenic plants having altered levels of delta-6 desaturase which
CC	in turn would alter the fatty acid composition. The enzyme is also useful
CC	for producing polyclonal or monoclonal antibodies. The polynucleotide
CC	is useful as primer or probe for screening cDNA libraries to
CC	isolate desired full-length cDNA clones.
XX	
Sequence	448 AA;
XX	

Search completed: August 9, 2001, 20:24:16
Job time: 250 sec

Query Match	93.4%	Score 71:	DB 21:	Length 422;
Best Local Similarity	92.3%	Pred. No. 0.00015;		
Matches 12; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GGLNQYIEHHLP	13	
Db	353	gglngyqjehhlp	365	

RESULT 15
AA71551

8

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 9, 2001, 20:25:07 ; Search time 45.84 Seconds
(without alignments)
5.839 Million cell updates/sec

Title: US-09-367-013B-2_COPY_390_402
Perfect score: 76
Sequence: 1 GGLNYQIEHLP 13

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: Issued_Patents_AA:*
2: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/6CTUS_COMB.pep:*
7: /cgn2_6/ptodata/2/1aa/6CTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	100.0	87	2	US-08-834-655-10
2	76	100.0	87	3	US-08-834-033A-11
3	76	100.0	87	4	US-09-363-574-10
4	76	100.0	355	2	US-08-834-655-5
5	76	100.0	355	3	US-08-834-033A-6
6	76	100.0	355	4	US-09-363-574-5
7	76	100.0	457	2	US-08-834-655-2
8	76	100.0	457	2	US-08-833-610-4
9	76	100.0	457	3	US-08-834-033A-2
10	76	100.0	457	3	US-08-834-033A-14
11	76	100.0	457	4	US-09-363-574-2
12	66	86.8	446	2	US-08-833-610-5
13	66	86.8	446	3	US-08-834-033A-15
14	64	84.2	131	2	US-08-834-655-9
15	64	84.2	131	3	US-08-834-033A-10
16	64	84.2	131	4	US-09-363-574-9
17	64	84.2	143	4	US-08-834-655-11
18	64	84.2	143	3	US-08-834-033A-12
19	64	84.2	143	4	US-09-363-574-11
20	64	84.2	359	1	US-08-367-382-2
21	64	84.2	359	1	US-08-366-779-2
22	64	84.2	359	1	US-08-478-727-2
23	64	84.2	359	1	US-08-473-508-2
24	64	84.2	359	1	US-08-789-936-2
25	64	84.2	359	2	US-08-833-610-6
26	64	84.2	359	3	US-08-834-033A-16
27	64	84.2	365	2	US-08-833-610-7

28	64	84.2	365	3	US-08-834-033A-17	Sequence 17, App1
29	60	78.9	448	1	US-08-366-779-5	Sequence 5, App1
30	60	78.9	448	1	US-08-789-936-5	Sequence 5, App1
31	58	76.3	125	2	US-08-834-655-8	Sequence 8, App1
32	58	76.3	125	3	US-08-834-033A-9	Sequence 9, App1
33	58	76.3	125	4	US-09-363-574-8	Sequence 8, App1
34	58	76.3	186	2	US-08-833-610-3	Sequence 3, App1
35	58	76.3	186	3	US-08-834-033A-13	Sequence 13, App1
36	58	76.3	446	2	US-08-833-610-2	Sequence 2, App1
37	58	76.3	446	3	US-08-834-033A-5	Sequence 5, App1
38	47	61.8	252	2	US-08-834-655-7	Sequence 7, App1
39	47	61.8	252	3	US-08-834-033A-8	Sequence 8, App1
40	47	61.8	252	4	US-09-363-574-7	Sequence 7, App1
41	41	53.9	268	2	US-08-611-880-2	Sequence 2, App1
42	38	50.0	22	2	US-08-488-161-16	Sequence 16, App1
43	38	50.0	22	3	US-09-273-685-16	Sequence 16, App1
44	38	50.0	22	5	PCT-US95-11934-16	Sequence 16, App1
45	38	50.0	23	1	US-08-176-500-27	Sequence 27, App1

ALIGNMENTS

RESULT 1
US-08-834-655-10
; Sequence 10, Application US/08834655
; Patent No. 5968809
GENERAL INFORMATION:
APPLICANT: KNOTZON, DEBORAH
APPLICANT: MURKERT, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P. C.
STREET: 260 SHERIDAN AVENUE, P. O. BOX 60039
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-Apr-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.124.00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-655-10
Query Match 100.0%; Score 76; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 9.3e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGLNVOIEHHLP 13
| | | | | | | | | |
DB 22 GGLNVOIEHHLP 34

RESULT 2

US-08-834-033A-11
; Sequence 11, Application US/08834033A
; Patent No. 6075183

GENERAL INFORMATION:

APPLICANT: KUTZON, DEBORAH
APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.

STREET: 2001 FERRY BUILDING

CITY: SAN FRANCISCO

STATE: CA

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/834,033A

FILING DATE: 11-APR-1997

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: WARD, MICHAEL R.

REGISTRATION NUMBER: 38, 651

REFERENCE/DOCKET NUMBER: CGAB-300.USA

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 433-4150

TELEFAX: (415) 433-8716

TELEX: N/A

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 87 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-834-033A-11

Query Match 100.0%; Score 76; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 9.3e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGLNVOIEHHLP 13
| | | | | | | | | |
DB 22 GGLNVOIEHHLP 34

RESULT 3

US-09-363-574-10
; Sequence 10, Application US/09363574
; Patent No. 6136574

GENERAL INFORMATION:

APPLICANT: KUTZON, DEBORAH

APPLICANT: MUKERJI, PRADIP

APPLICANT: HUANG, YUNG-SHENG

APPLICANT: THURMOND, JENNIFER

APPLICANT: CHAUDHARY, SUNITA

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/363,574

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: WARD, MICHAEL R.

REGISTRATION NUMBER: 38, 651

REFERENCE/DOCKET NUMBER: CGAB-202 USA

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 433-4150

TELEFAX: (415) 433-8716

TELEX: N/A

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 87 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-363-574-10

Query Match 100.0%; Score 76; DB 4; Length 87;
Best Local Similarity 100.0%; Pred. No. 9.3e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGLNVOIEHHLP 13
| | | | | | | | | |
DB 22 GGLNVOIEHHLP 34

RESULT 4

US-08-834-655-5
; Sequence 5, Application US/08834655
; Patent No. 5968809

GENERAL INFORMATION:

APPLICANT: KUTZON, DEBORAH

APPLICANT: MUKERJI, PRADIP

APPLICANT: HUANG, YUNG-SHENG

APPLICANT: THURMOND, JENNIFER

APPLICANT: CHAUDHARY, SUNITA

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: RAE-VENTER LAW GROUP, P.C.

STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039

CITY: PALO ALTO

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/834,655

FILING DATE: 11-APR-1997

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.124.00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-655-5

Query Match 100.0%; Score 76; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGLNYQIEHHLP 13
|||||
Db 288 GGLNYQIEHHLP 300

RESULT 5
US-08-834-033A-6
Sequence 6, Application US/08834033A
Patent No. 6075183
GENERAL INFORMATION:
APPLICANT: KNUFTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YONG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,033A
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300.USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-033A-6

Query Match 100.0%; Score 76; DB 3; Length 355;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGLNYQIEHHLP 13
|||||
Db 288 GGLNYQIEHHLP 300

RESULT 6
US-09-363-574-5
Sequence 5, Application US/09363574
Patent No. 6136574
GENERAL INFORMATION:
APPLICANT: KNUFTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YONG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,574
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-202 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-363-574-5

Query Match 100.0%; Score 76; DB 4; Length 355;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGLNYQIEHHLP 13
|||||
Db 288 GGLNYQIEHHLP 300

RESULT 7
US-08-834-655-2
Sequence 2, Application US/08834655
Patent No. 5968809
GENERAL INFORMATION:
APPLICANT: KNUFTZON, DEBORAH

APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.124.00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-655-2

Query Match 100.0%; Score 76; DB 2; Length 457;
Best Local Similarity 100.0%; Pred. No. 6.2e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGLNYOIEHHLP 13
|||||

Db 390 GGLNYOIEHHLP 402

RESULT 8
US-08-833-610-4
Sequence 4, Application US/08833610
Patent No. 5972664
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,610
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.123.00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)328-4400
TELEFAX: (650)328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-833-610-4

Query Match 100.0%; Score 76; DB 2; Length 457;
Best Local Similarity 100.0%; Pred. No. 6.2e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGLNYOIEHHLP 13
|||||

Db 390 GGLNYOIEHHLP 402

RESULT 9
US-08-834-033A-2
Sequence 2, Application US/08834033A
Patent No. 6075183
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,033A
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300.USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids

TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-033A-2

Query Match 100.0%; Score 76; DB 3; Length 457;
Best Local Similarity 100.0%; Pred. No. 6.2e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGLNYQIEHHLP 13
|||||
Db 390 GGLNYQIEHHLP 402

RESULT 10
US-08-834-033A-14
Sequence 14, Application US/08834033A
Patent No. 6075183
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERT, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,033A
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300,USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-033A-14

Query Match 100.0%; Score 76; DB 3; Length 457;
Best Local Similarity 100.0%; Pred. No. 6.2e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGLNYQIEHHLP 13
|||||
Db 390 GGLNYQIEHHLP 402

RESULT 11

US-09-363-574-2
Sequence 2, Application US/09363574
Patent No. 6136574
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERT, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,574
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-202 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-363-574-2

Query Match 100.0%; Score 76; DB 4; Length 457;
Best Local Similarity 100.0%; Pred. No. 6.2e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGLNYQIEHHLP 13
|||||
Db 390 GGLNYQIEHHLP 402

RESULT 12
US-08-833-610-5
Sequence 5, Application US/08833610
Patent No. 5972664
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERT, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CALIFORNIA

COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,610
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.123.0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)328-4400
TELEFAX: (650)328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-833-610-5

Query Match 86.8%; Score 66; DB 2; Length 446;
Best Local Similarity 84.6%; Pred. No. 0.00037;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGLNVOIEHHLP 13
|||:|||||||
Db 368 GGLQFOIEHHLP 380

RESULT 13
US-08-834-033A-15
Sequence 15, Application US/08834033A
Patent No. 6075183
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERT, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,033A
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300. USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150

TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-033A-15

Query Match 86.8%; Score 66; DB 3; Length 446;
Best Local Similarity 84.6%; Pred. No. 0.00037;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGLNVOIEHHLP 13
|||:|||||||
Db 368 GGLQFOIEHHLP 380

RESULT 14
US-08-834-655-9
Sequence 9, Application US/08834655
Patent No. 5968809
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERT, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.124.0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-655-9

Query Match 84.2%; Score 64; DB 2; Length 131;
Best Local Similarity 84.6%; Pred. No. 0.00021;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGLNVOIEHHLP 13

Db 89 GHLNFOIEHHLP 101

RESULT 15

US-08-834-033A-10
 ; Sequence 10, Application US/08834033A
 ; Patent No. 6075183
 ; GENERAL INFORMATION:
 ; APPLICANT: KNUITZON, DEBORAH
 ; APPLICANT: MUKERJI, PRADIP
 ; APPLICANT: HUANG, YONG-SHENG
 ; APPLICANT: THURMOND, JENNIFER
 ; APPLICANT: CHAUDHARY, SUNITA
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 ; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
 ; STREET: 2001 FERRY BUILDING
 ; CITY: SAN FRANCISCO
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WORDPERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/834,033A
 ; FILING DATE: 11-APR-1997
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WARD, MICHAEL R.
 ; REGISTRATION NUMBER: 38,651
 ; REFERENCE/DOCKET NUMBER: CGAB-300.USA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 433-4150
 ; TELEFAX: (415) 433-8716
 ; TELEX: N/A
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 131 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-834-033A-10

Query Match 84.2%; Score 64; DB 3; Length 131;
 Best Local Similarity 84.6%; Pred. No. 0.00021;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 1 GGLNYQIEHHLP 13
 | ||:|||||||
 Db 89 GHLNFOIEHHLP 101

Search completed: August 9, 2001, 20:25:07
 Job time: 206 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 9, 2001, 20:26:07 ; Search time 50.69 Seconds
(without alignments)
19.536 Million cell updates/sec

Title: US-09-367-013b-2_COPY_390_402

Perfect score: 76
Sequence: 1 GGLNYQIEHHLP 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76	100.0	447	1 T43319	Delta5 fatty acid
2	76	100.0	473	1 T26280	linoleoyl-CoA desaturase
3	71	93.4	345	2 T36617	probable Delta6 fatty acid
4	64	84.2	359	2 S35157	Delta6 fatty acid
5	64	84.2	368	2 S54809	linoleoyl-CoA desaturase
6	64	84.2	444	2 T13155	linoleoyl-CoA desaturase
7	64	84.2	444	2 JG0180	Delta6 fatty acid
8	64	84.2	449	2 A84900	hypothetical protein
9	64	84.2	449	2 T47950	delta-8 sphingolipid
10	64	84.2	449	2 T50355	delta-8 sphingolipid
11	64	84.2	458	2 S68358	Delta6 sphingolipid
12	58	76.3	523	3 JG7556	linoleoyl-CoA desaturase
13	57	75.0	370	2 B83034	conserved hypothetical protein
14	53	69.7	427	2 G70590	probable desaturase
15	45	59.2	287	2 T11959	hypothetical protein
16	45	59.2	369	2 S75038	hypothetical protein
17	44	57.9	140	2 G82323	conserved hypothetical protein
18	44	57.9	312	2 S77365	hypothetical protein
19	44	57.9	550	2 C86704	conserved hypothetical protein
20	41.5	54.6	211	2 T11220	reverse transcriptase
21	41.5	54.6	362	2 T40333	probable fatty acid
22	41	53.9	214	2 JG5646	interleukin-1 beta
23	41	53.9	241	2 T01936	probable ethylene
24	41	53.9	300	2 T27158	hypothetical protein
25	41	53.9	350	2 T29409	hypothetical protein
26	41	53.9	360	2 T32554	hypothetical protein
27	41	53.9	413	2 D85387	probable synthetase
28	41	53.9	413	2 E64815	yeast protein - Esc
29	40	52.6	309	2 T31123	hypothetical protein

30	40	52.6	482	2 S22654	ARS-binding factor
31	40	52.6	744	2 B64049	outer membrane protein
32	39.5	52.0	674	2 S32230	Ca2+-transporting
33	39.5	52.0	1003	2 S07526	Ca2+-transporting
34	39.5	52.0	1142	2 T39103	probable negative
35	39	51.3	320	2 F96745	unknown protein T9
36	39	51.3	325	2 F86605	sulfite synthetase/
37	39	51.3	325	2 G72020	3' (2'), 5'-bisphosph
38	39	51.3	373	2 S65583	maturing type protei
39	39	51.3	382	2 D72513	probable aminopept
40	39	51.3	405	1 Q08E35	BRRF3 protein - hu
41	39	51.3	685	2 C70678	probable electron
42	39	51.3	988	1 S35362	protein kinase C (
43	39	51.3	4056	2 H96599	protein F14J16.10
44	38.5	50.7	333	2 T26230	hypothetical prote
45	38.5	50.7	367	2 S55961	hypothetical prote

ALIGNMENTS

```
RESULT 1
T43319
Delta5 fatty acid desaturase (EC 1.14.99.-) T13F2.1 [validated] - Caenorhabditis eleg
C:Species: Caenorhabditis elegans
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
R:Michaelson, L.V.; Napier, J.A.; Lewis, M.; Griffiths, G.; Lazarus, C.M.; Stobart, A
FEBS Lett. 439, 215-218, 1998
A:Title: Functional identification of a fatty acid delta5 desaturase gene from Caenor
A:Reference number: 222422; MUID:99059458
A:Accession: T43319
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-447 <MTC>
A:Cross-references: EMBL:AF078796; NID:94003522; PIDN:AAC95143.1; PID:94003523
R:Swindburne, J.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19947
A:Accession: T24875
A:Status: translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-197, 'VSHIENN', 198-447 <MTC>
A:Cross-references: EMBL:Z81122; PIDN:CAB03352.1; GSPDB:GND00022; CESP:T13F2.1
A:Experimental source: clone T13F2
A:Genetics:
A:Gene: CESP:T13F2.1; des-5
A:Map position: 4
A:Introns: 43/3; 80/3; 197/3; 295/3; 318/2; 349/1; 384/3
C:Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 100.0%; Score 76; DB 1; Length 447;
Best local similarity 100.0%; Pred. No. 8.5e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGLNYQIEHHLP 13
Db 379 GGLNYQIEHHLP 391

RESULT 2
T26280
linoleoyl-CoA desaturase (EC 1.14.99.25) W08D2.4 - Caenorhabditis elegans
N:Alternative names: Delta6 fatty acid desaturase
C:Species: Caenorhabditis elegans
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
A:Accession: T26280; T37238
R:Swindburne, J.; Almscough, R.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z20188
A:Accession: T26280
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A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-473 <MID>
A:Cross-references: EMBL:Z70271; PIDN:CAA94233.1; GSPDB:GN00022; CESP:W08D2.4
A:Experimental source: clone W08D2
R:Mapler, J.A.; Hey, S.J.; Lacey, D.J.; Shewry, P.R.
Biochem. J. 330, 611-614, 1998
A:Title: Identification of a *Caenorhabditis elegans* Delta6-fatty-acid-desaturase by heteroduplex analysis
A:Reference number: Z21637; MUID:98149727
A:Accession: T37238
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-38, 69-430, 'V', 432-473 <NAP>
A:Cross-references: EMBL:AF031477; MID:g3088519; PIDN:AAC15586.1; PID:g3088520
C:Genetics:
A:Gene: CESP:W08D2.4
A:Map position: 4
A:introns: 13/3; 39/2; 234/3; 277/3; 378/1; 413/3
A:Superfamily: *Caenorhabditis elegans* Delta6 fatty acid desaturase
C:Keywords: alternative splicing; oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 100.0%; Score 76; DB 1; Length 473;
Best Local Similarity 100.0%; Pred. No. 9.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGLNYQIEHHLP 13
|||||
Db 408 GGLNYQIEHHLP 420

RESULT 3
T3617
probable Delta6 fatty acid desaturase (EC 1.14.99.-) SCH35.42c [similarity] - Streptomyces
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence-revision 03-Dec-1999 #text-change 20-Jun-2000
C:Accession: T3617
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A:Reference number: Z21610
A:Accession: T3617
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-345 <OLI>
A:Cross-references: EMBL:AL078610; PIDN:CAB44385.1; GSPDB:GN00070; SCOEDB:SC35.42c
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC35.42c
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 93.4%; Score 71; DB 2; Length 345;
Best Local Similarity 92.3%; Pred. No. 5e-05;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGLNYQIEHHLP 13
|||||
Db 278 GGLNYQIEHHLP 290

RESULT 4
S35157
Delta6 fatty acid desaturase (EC 1.14.99.-) [Imported] - *Synechocystis* sp.
C:Species: *Synechocystis* sp.
C:Date: 19-Mar-1997 #sequence-revision 19-Mar-1997 #text-change 20-Jun-2000
C:Accession: S35157; S76243
R:Reddy, A.S.; Nuccio, M.L.; Gross, L.M.; Thomas, T.L.
Plant Mol. Biol. 22, 293-300, 1993
A:Title: Isolation of a Delta(6)-desaturase gene from the cyanobacterium *Synechocystis* sp.
A:Reference number: S35157; MUID:9328363
A:Accession: S35157
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-359 <RED>
A:Cross-references: GB:L11421; MID:g349562; PIDN:AAZ7286.1; PID:g349563
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O.; Kikuchi, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, K.
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.
A:Reference number: S74322; MUID:97061201
A:Accession: S76243
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-359 <KAN>
A:Cross-references: EMBL:D90914; GB:AB001339; MID:g1653477; PIDN:BAA18502.1; PID:d101
A:Experimental source: PCC 6803
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 84.2%; Score 64; DB 2; Length 359;
Best Local Similarity 76.9%; Pred. No. 0.00095;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGLNYQIEHHLP 13
|||||
Db 298 GGLNYQIEHHLP 310

RESULT 5
S54809
linoleoyl-CoA desaturase (EC 1.14.99.25) - *Spirulina platensis*
N:Alternate names: Delta6-desaturase
C:Species: *Spirulina platensis*
C:Date: 08-Jul-1995 #sequence-revision 21-Jul-1995 #text-change 09-Jun-2000
C:Accession: S54809
R:Itasaka, Y.
submitted to the EMBL Data Library, May 1995
A:Reference number: S54809
A:Accession: S54809
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-368 <TAS>
A:Cross-references: EMBL:X87094; MID:g809109; PIDN:CAA60573.1; PID:g809110
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 84.2%; Score 64; DB 2; Length 368;
Best Local Similarity 84.6%; Pred. No. 0.00097;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGLNYQIEHHLP 13
|||||
Db 297 GGLNYQIEHHLP 309

RESULT 6
T13155
linoleoyl-CoA desaturase (EC 1.14.99.25) [validated] - human
N:Alternate names: Delta6 fatty acid desaturase; protein DFFP586C201.1
C:Species: *Homo sapiens* (man)
C:Date: 13-Aug-1999 #sequence-revision 13-Aug-1999 #text-change 09-Jun-2000
C:Accession: T13155; T08765
R:Cho, H.P.; Nakamura, M.T.; Clarke, S.D.
J. Biol. Chem. 274, 471-477, 1999
A:Title: Cloning, expression, and nutritional regulation of the mammalian Delta-6 desaturase
A:Reference number: Z17612; MUID:99085046
A:Accession: T13155
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-444 <CHO>
A:Cross-references: EMBL:AF126799; MID:g4406527; PID:g4406528; PIDN:AAD20018.1
R:Mamuti, R.; Heudner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, March 1999
A:Reference number: Z16471

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A:Accession: T08765
A:Molecule type: mRNA
A:Residues: 'RTRG', 138-428, 'D', 430, 'M', 432-444 <WAM>
A:Cross-references: EMBL:AL050118
A:Experimental source: adult uterus; clone DKFZ586C201
C:Genetics:
A:Gene: GDB:FADSD6
A:Cross-references: GDB:9956652
A:Note: DKFZ586C201.1
C:Superfamily: cytochrome b5 core homology
C:Keywords: cytochrome b5 core homology <CB5>
F:18-94/Domain: cytochrome b5 core homology <CB5>
F:53/6/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match          84.2%  Score 64:  DB 2:  Length 444:
Best Local Similarity 84.6%  Pred. No. 0.0012:
Matches 11:  Conservative 1:  Mismatches 1:  Indels 0:  Gaps 0:

QY 1 GGLNYQIEHHLFP 13
DB 377 GHLNFOIEHHLFP 389

RESULT 7
JG0180
Delta6 fatty acid desaturase (EC 1.14.99.-) [Imported] - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
C:Accession: JG0180
R:Akl, T., Shimada, Y., Inagaki, K., Higashimoto, H., Kawamoto, S., Shigeta, S., Ono, K.,
Biochem. Biophys. Res. Commun. 255, 575-579, 1999
A:Title: Molecular cloning and functional characterization of rat delta-6 fatty acid des
A:Reference number: JG0180, MUID:99160394
A:Accession: JG0180
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-444 <AKI>
A:Cross-references: DDBJ:AB021980; NID:94514721; PIDN:BAW5496.1; PID:94514722
C:Superfamily: cytochrome b5 core homology
C:Keywords: heme; iron; metalloprotein; oxidoreductase; unsaturated fatty acid biosynthe
F:18-94/Domain: cytochrome b5 core homology <CB5>
F:53/6/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match          84.2%  Score 64:  DB 2:  Length 444:
Best Local Similarity 84.6%  Pred. No. 0.0012:
Matches 11:  Conservative 1:  Mismatches 1:  Indels 0:  Gaps 0:

QY 1 GGLNYQIEHHLFP 13
DB 377 GHLNFOIEHHLFP 389

RESULT 8
AB4900
hypothetical protein At2g46210 [Imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: AB4900
R:Lin, X., Kaul, S., Rounsley, S.D., Shea, T.P., Benito, M.I., Town, C.D., Fujii, C.Y.,
M., Koo, H., Moffatt, K.S., Cronin, L.A., Shen, M., VanAken, S.E., Umayam, L., Tallon, L.,
Neus, D., Nierman, W.C., White, O., Eisen, J.A., Salzberg, S.L., Fraser, C.M., Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: AB4420; MUID:20083487
A:Accession: AB4900
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-449 <STO>
A:Cross-references: GB:AE002093; NID:93702328; PIDN:AMC62885.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g46210

A:Map position: 2

Query Match          84.2%  Score 64:  DB 2:  Length 449:
Best Local Similarity 76.9%  Pred. No. 0.0012:
Matches 10:  Conservative 2:  Mismatches 1:  Indels 0:  Gaps 0:

QY 1 GGLNYQIEHHLFP 13
DB 369 GGLQFOLEHHLFP 381

RESULT 9
T47950
delta-8 sphingolipid desaturase (EC 1.14.99.-) [validated] - Arabidopsis thaliana
N:Alternate names: protein F2A19.180
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C:Accession: T47950; T51848
R:De Haan, M., Maarse, A.C., Grivell, L.A., Mewes, H.W., Lemcke, K., Mayer, K.F.X., Q
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z24480
A:Accession: T47950
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-449 <DEH>
A:Cross-references: EMBL:AL132962; PIDN:CAB71088.1
A:Experimental source: cultivar Columbia; BAC clone F2A19
R:Spertling, P., Zaehneringer, U., Heinz, E.
J. Biol. Chem. 273, 28590-28596, 1998
A:Title: A sphingolipid desaturase from higher plants. Identification of a new cytoch
A:Reference number: Z22986; MUID:99003197
A:Accession: T51848
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-449 <SPE>
A:Cross-references: EMBL:AJ224161; PIDN:CAI11858.1
A:Experimental source: cultivar Columbia; mainly green parts, some flowers, few roots
C:Genetics:
A:Gene: slid1
A:Map position: 3
A:Note: F2A19.180
C:Function:
A:Description: (EC 1.14.99.-): delta-8 sphingolipid desaturase [validated; MUID:99003
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match          84.2%  Score 64:  DB 2:  Length 449:
Best Local Similarity 76.9%  Pred. No. 0.0012:
Matches 10:  Conservative 2:  Mismatches 1:  Indels 0:  Gaps 0:

QY 1 GGLNYQIEHHLFP 13
DB 369 GGLQFOLEHHLFP 381

RESULT 10
T50555
delta-8 sphingolipid desaturase [Imported] - rape
C:Species: Brassica napus (rape)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 15-Sep-2000
C:Accession: T50555
R:Spertling, P., Zaehneringer, U., Heinz, E.
J. Biol. Chem. 273, 28590-28596, 1998
A:Title: A sphingolipid desaturase from higher plants. Identification of a new cytoch
A:Reference number: Z22986; MUID:99003197
A:Accession: T50555
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-449 <SPE>
A:Cross-references: EMBL:AJ224160; PIDN:CAI11857.1
A:Experimental source: cultivar Drakkar
C:Genetics:
```


A;Molecule type: DNA
 A;Residues: 1-287 <GLO>
 A;Cross-references: EMBL:AF022186; NID:g2465730; PID:AB82698.1; PID:g2465769
 A;Experimental source: strain RK1
 C:Genetics:
 A;Gene: desa
 A;Genome: chloroplast
 C;Keywords: chloroplast

Query Match 59.2%; Score 45; DB 2; Length 287;
 Best Local Similarity 58.3%; Pred. No. 1.9;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 GLNYQIEHLEP 13
 | | | : | | | : |
 Db 227 GQNHLYVHLEP 238

Search completed: August 9, 2001, 20:26:08
 Job time: 247 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 9, 2001, 20:36:51 ; Search time 28.86 Seconds
(without alignments)
15.430 Million cell updates/sec

Title: US-09-367-013b-2_COPY_390_402
Perfect score: 76
Sequence: 1 GGLNYQIEHLEFP 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	84.2	359	1	LLCD_SYNY3
2	41	53.9	268	1	ILIB_HORSE
3	41	53.9	413	1	YBHO_ECOLI
4	40	52.6	486	1	BAFL_KLULA
5	40	52.6	744	1	HXCL_HAEIN
6	39.5	52.0	1003	1	ATC_AKTSE
7	39	51.3	373	1	MATC_NEOCR
8	39	51.3	405	1	VGLM_EBV
9	39	51.3	988	1	PCK1_SCHPO
10	38.5	50.7	367	1	YL05_YEAST
11	38	50.0	160	1	RS7_RICPR
12	38	50.0	291	1	ATP6_MAIZE
13	38	50.0	502	1	YH60_MYTU
14	38	50.0	844	1	AMPN_LACHE
15	38	50.0	964	1	UL70_MCVS
16	37.5	49.3	229	1	Y997_HAEIN
17	37	48.7	238	1	CDSA_RICPR
18	37	48.7	330	1	YB40_MERJA
19	37	48.7	363	1	YLOM_BACSU
20	37	48.7	662	1	YAE8_YEAST
21	37	48.7	3137	1	CA36_CHICK
22	36	47.4	242	1	CRTW_AGRAU
23	36	47.4	242	1	CRTW_AICSP
24	36	47.4	248	1	IFE3_CAEEL
25	36	47.4	263	1	IFE3_CAEEL
26	36	47.4	314	1	PANB_BUCAI
27	36	47.4	359	1	YFCB_HAEIN
28	36	47.4	375	1	OM40_MOUSE
29	36	47.4	475	1	MRK1_YEAST
30	36	47.4	498	1	SYC_AERPE
31	36	47.4	595	1	SG28_BPMD2
32	36	47.4	595	1	VG28_BPMD5
33	36	47.4	835	1	SMI3_YEAST

34	35.5	46.7	428	1	G6NT_HUMAN	002742 homo sapien
35	35.5	46.7	580	1	Y686_MERJA	058099 methanococc
36	35	46.1	104	1	YR7H_ECOLI	P21322 escherichia
37	35	46.1	107	1	YECR_ECOLI	P76308 escherichia
38	35	46.1	138	1	YJGD_ECOLI	P27163 escherichia
39	35	46.1	138	1	YJGD_SALTY	008019 salmonella
40	35	46.1	153	1	Y587_MERJA	058007 methanococc
41	35	46.1	155	1	RS7_THERM	P17291 thermus aqu
42	35	46.1	303	1	META_BACHD	09KAK7 bacillus ha
43	35	46.1	310	1	AP1_CHICK	P18870 gallus gall
44	35	46.1	313	1	AP1_COTUA	P12961 coturnix co
45	35	46.1	328	1	GALE_CORDI	P33119 corynebacte

ALIGNMENTS

RESULT	ID	LLCD_SYNY3	STANDARD	PRT	359 AA
AC	008871	LLCD_SYNY3			
DT	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	01-NOV-1997	(Rel. 35, Last annotation update)			
DE	LINOLOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESATURASE).				
GN	DES6 OR SLD0262.				
OS	Synechocystis sp. (strain PCC 6803).				
OC	Bacteria; Cyanobacteria; Chroococcales; Synechocystis.				
OX	NCBI_TaxID=1148;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=93283633; PubMed=8389613;				
RA	Reddy A.S., Nuccio M.L., Gross L.M., Thomas T.L.;				
RT	"Isolation of a delta 6-desaturase gene from the cyanobacterium				
RT	Synechocystis sp. strain PCC 6803 by gain-of-function expression in				
RT	Anabaena sp. strain PCC 7120."				
RL	Plant Mol. Biol. 22:293-300(1993).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=97061201; PubMed=8905231;				
RA	Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,				
RA	Miyajima N., Hirosewa M., Sugiyura M., Sasamoto S., Kimura T.,				
RA	Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,				
RA	Okumura S., Shimo S., Takeuchi C., Wada T., Watanabe A.,				
RA	Yamada M., Yasuda M., Tabata S.;				
RT	"Sequence analysis of the genome of the unicellular cyanobacterium				
RT	Synechocystis sp. strain PCC6803. II. Sequence determination of the				
RT	entire genome and assignment of potential protein-coding regions."				
RL	DNA Res. 3:109-136(1996).				
CC	-1- CATALYTIC ACTIVITY: LINOLOYL-COA + AH(2) + O(2) -> GAMMA-				
CC	LINOLOYL-COA + A + 2 H(2)O.				
CC	-1- COFACTOR: IRON.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; L11421; AAA27286.1; -				
DR	EMBL; D90914; BAA18502.1; -				
KW	Oxidoreductase; Iron.				
SO	SEQUENCE 359 AA; 41425 MW; 33FB165AEB98C05F CRC64;				

Query Match 84.2% Score 64; DB 1; Length 359;

Best Local Similarity 76.9%; Pred. No. 0.00091; Indels 0; Gaps 0;

Matches 10; Conservative 2; Mismatches 1;

1 GGLNYQIEHLEFP 13

|||||:||||

Db 298 GGLNHOVTHHLFP 310

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RESULT 2
IL1B_HORSE STANDARD: PRT; 268 AA.
ID IL1B_HORSE 028386; 077744; 018995;
AC 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
GN IL1B.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN RP SEQUENCE FROM N.A.
RX MEDLINE-96131982; PubMed-8578682;
RA Kato H., Ohashi T., Nakamura N., Nishimura Y., Watari T., Gotsuka R.,
RA Tsujimoto H., Hasegawa A.;
RT "Molecular cloning of equine interleukin-1 alpha and -beta cDNAs.";
RL Vet. Immunol. Immunopathol. 48:221-231(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-98285941; PubMed-9622738;
RA Howard R.D., McIlwraith C.W., Trotter G.W., Nyborg J.K.;
RT "Cloning of equine interleukin-1 alpha and equine interleukin-1 beta
RT and determination of their full-length cDNA sequences.";
RL Am. J. Vet. Res. 59:704-711(1998).
RN [3]
RP SEQUENCE FROM N.A. (SHORT FORM).
RX MEDLINE-97080493; PubMed-8921838;
RA Kato H., Yoon H.Y., Ohashi T., Watari T., Gotsuka R., Tsujimoto H.,
RA Hasegawa A.;
RT "Identification of an alternatively spliced transcript of equine
RT interleukin-1 beta.";
RL Gene 177:11-16(1996).
RN [1]
RP FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES. IL-1 STIMULATES
THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS
(BY SIMILARITY).
CC -1 SUBUNIT: MONOMER. (BY SIMILARITY).
CC -1 ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1 DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -1 SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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CC -----
CC EMBL: D42147; BAA07718.1; -
CC EMBL: U92481; AAC9256.1; -
CC EMBL: D42165; BAA2528.1; -
CC InterPro: IPR000975; -
CC InterPro: IPR002348; -
CC pfam: PF00340; interleukin-1; 1.
CC PRINTS: PR00262; IL1HGF.
CC PRINTS: PR00264; INTERLEUKIN1.
CC PROSITE: PS00253; INTERLEUKIN_1; 1.

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KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen;
KM Alternative splicing.
FT PROPEP 1 115 BY SIMILARITY.
FT CHAIN 116 268 INTERLEUKIN-1 BETA.
FT VARSPLIC 101 154 MISSING (IN SHORT ISOPFORM).
FT CONFLICT 45 45 D -> N (IN REF. 2).
FT CONFLICT 55 55 H -> Q (IN REF. 2).
FT CONFLICT 64 65 AM -> VV (IN REF. 2).
FT CONFLICT 71 71 V -> M (IN REF. 2).
FT CONFLICT 110 111 EG -> DD (IN REF. 2).
FT CONFLICT 118 118 M -> V (IN REF. 2).
FT CONFLICT 245 245 S -> K (IN REF. 2).
SQ SEQUENCE 268 AA; 30268 MW; 336F27792A1542EA CRC64;

Query Match 53.9%; Score 41; DB 1; Length 268;
Best Local Similarity 50.0%; Pred. No. 6;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGLNHOVTHHLFP 12
DB 46 GGIQLOPSSHLY 57

RESULT 3
YBHO_ECOLI STANDARD: PRT; 413 AA.
ID YBHO_ECOLI
AC P75771;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HYPOTHEICAL 47.6 KDA PROTEIN IN MOAE-RHLE INTERGENIC REGION.
GN YBHO.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE-97426617; PubMed-9278503;
RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE-97061202; PubMed-8905232;
RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto S., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horinouchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
RN [1]
RP SIMILARITY: BELONGS TO THE PHOSPHOLIPASE D FAMILY. CARDIOLIPIN
CC SYNTHASE SUBFAMILY.
CC -----
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CC -----
CC EMBL: AE000181; AAC73876.1; -
CC EMBL: D90716; BAA35448.1; -

```

DR EcGene; EG13671; ybho.
 DR InterPro; IPR001736; .
 DR Pfam; PF00614; PLDC; 2.
 KW Hypothetical protein; Transferase.
 SQ SEQUENCE 413 AA; 47633 MM; 74998B2A1AD24A11 CRC64;

Query Match 53.9%; Score 41; DB 1; Length 413;
 Best Local Similarity 77.8%; Pred. No. 9.2;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGLNYQIEH 9
 |||||
 Db 127 GGLNYSAEH 135

RESULT 4
 BAF1_KLUFA STANDARD; PRT; 486 AA.
 ID BAF1_KLUFA
 AC P26375;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE TRANSCRIPTION FACTOR BAF1 (ARS BINDING FACTOR 1) (PROTEIN ABF1)
 DE (BIDIRECTIONALLY ACTING FACTOR).
 GN ABF1.
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_Taxid=28985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140;
 RX MEDLINE=92279012; PubMed=1594441;
 RA Goncalves P.M., Maurer K., Mager W.H., Planta R.J.;
 RT "Kluyveromyces contains a functional ABF1-homologue";
 RL Nucleic Acids Res. 20:2211-2215(1992).
 RP REVISIONS TO C-TERMINUS.
 RX MEDLINE=93277959; PubMed=7916634;
 RA Oebye E.H.H., Maurer K., Mager W.H., Planta R.J.;
 RT "Structure of the ABF1-homologue from Kluyveromyces marxianus";
 RL Biochim. Biophys. Acta 1173:233-236(1993).
 CC -1- FUNCTION: TRANS-ACTING FACTOR IN THE REGULATION OF TRANSCRIPTION
 AND IN DNA REPLICATION. INVOLVED IN THE TRANSCRIPTION ACTIVATION
 OF A SUBSET OF RIBOSOMAL PROTEINS GENES. BINDS THE ARS-ELEMENTS
 CC FOUND IN MANY PROMOTERS. BINDS TO THE SEQUENCE 5'-TCN(?)AGC-3'.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- PTM: EXTENSIVELY PHOSPHORYLATED ON SER AND THR RESIDUES
 CC (BY SIMILARITY).
 CC -1- SIMILARITY: STRONG TO YEAST BAF1, AND LOCAL TO YEAST RAP1.
 CC -----
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 CC -----
 CC EMBL; X64462; CAA45792.1; .
 DR PIR; S22654; S22654.
 DR TRANSFAC; T01240; .
 KW Transcription regulation; Activator; DNA-binding; Nuclear protein;
 KW Phosphorylation; Zinc-finger; Metal-binding; Zinc; DNA replication;
 KW Trans-acting factor.
 FT ZN_FING 47 CHC2-TYPE.
 FT ZN_FING 121 130 ASP/GLU-RICH.
 FT MOD_RES 392 392 PHOSPHORYLATION (BY PKC) (POTENTIAL).
 SQ SEQUENCE 486 AA; 55042 MM; E5CF6056EA901A6 CRC64;

Query Match 52.6%; Score 40; DB 1; Length 486;

Best Local Similarity 46.2%; Pred. No. 16;
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGLNYQIEHHLFP 13
 ||::||:|
 Db 267 GGDHQQVOHHHP 279

RESULT 5
 HXCL_HAETN STANDARD; PRT; 744 AA.
 ID HXCL_HAETN
 AC P44523;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HEME/HEMOPEXIN UTILIZATION PROTEIN C PRECURSOR.
 GN HXUC OR H10113.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 OX NCBI_Taxid=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RD / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-T., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Sauder D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RT Rd.";
 RL Science 269:496-512(1995).
 CC -1- FUNCTION: REQUIRED FOR UTILIZATION OF FREE HEME AT LOW
 CC CONCENTRATIONS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: OUTER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
 CC -1- SIMILARITY: LOW, TO THE CORRESPONDING PROTEIN IN SEROTYPE B OF
 CC H. INFLUENZAE.
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 CC -----
 CC EMBL; U32696; AAC21789.1; .
 DR TIGR; H10113; .
 DR InterPro; IPR000531; .
 DR Pfam; PF00593; TonB_boxC; 1.
 DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; FALSE_NEG.
 DR PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
 KW Outer membrane; Transport; TonB box; Signal; Receptor.
 FT SIGNAL 1
 FT CHAIN 1 744 HEME/HEMOPEXIN UTILIZATION PROTEIN C.
 FT SIGNAL 1
 SQ SEQUENCE 744 AA; 85043 MM; 7AD94EF72A1AEC31 CRC64;

Query Match 52.6%; Score 40; DB 1; Length 744;
 Best Local Similarity 60.0%; Pred. No. 25;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 GGLNYQIEHHL 11
 ||||:|:|
 Db 473 GGLNDVNHYL 482

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RESULT 6
ATC_ARTSF STANDARD: PRT: 1003 AA.
ID ATC_ARTSF
AC P35316;
DT 01-FEB-1994 (rel. 28, Created)
DT 01-FEB-1994 (rel. 28, Last sequence update)
DT 01-JUN-1994 (rel. 29, Last annotation update)
DE CALCIUM-TRANSPORTING ATPASE SARCOPLASMIC/ENDOPLASMIC RETICULUM TYPE
DE (EC 3.6.1.38) (CALCIUM PUMP).
OS Artemia salinifranciscana (Brine shrimp) (Artemia franciscana).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;
OC Artemiidae; Artemia.
OX NCBI_Taxid=6661;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90133927; PubMed=2533270;
RA Palmero I., Sastre L.;
RT "Complementary DNA cloning of a protein highly homologous to
RT mammalian sarcoplasmic reticulum Ca-ATPase from the crustacean
RT Artemia."
RT J. Mol. Biol. 210:737-748(1989).
RN [2]
RP SEQUENCE OF 354-1003 FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=93300797; PubMed=8314776;
RA Escalante R., Sastre L.;
RT "Similar alternative splicing events generate two sarcoplasmic or
RT endoplasmic reticulum Ca-ATPase isoforms in the crustacean Artemia
RT franciscana and in vertebrates."
RT J. Biol. Chem. 268:14090-14095(1993).
CC -1- FUNCTION: THIS MAGNESIUM DEPENDENT ENZYME CATALYZES THE
CC HYDROLYSIS OF ATP COUPLED WITH THE TRANSPORT OF THE CALCIUM.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + ORTHOPHOSPHATE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SARCOPLASMIC
CC RETICULUM.
CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING. THE 2 FORMS DIFFER ONLY IN THEIR C-TERMINAL AMINO ACIDS.
CC THE LONGER FORM PRESENTS AN EXTENSION, A POTENTIAL TRANSMEMBRANE
CC DOMAIN, WHICH MAY HAVE AN IMPORTANT FUNCTIONAL ROLE.
CC -1- DEVELOPMENTAL STAGE: ISOFORM 2 (LONG FORM) IS EXPRESSED ONLY IN
CC EARLY STAGES OF EMBRYONIC DEVELOPMENT (CYSTS), WHILE ISOFORM 1
CC (SHORT FORM) IS ALSO FOUND IN LATER EMBRYONIC STAGES AND ADULTS.
CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
CC (E1-E2 ATPASES).
-----
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-----
CC EMBL: X51674; CAA35980.1; -
CC EMBL: X72713; CAA51262.1; -
CC PIR: S07526; S07526.
CC Interpro: IPR001757; -
CC Pfam: PF001122; E1-E2_ATPase; 1.
CC PRINTS: PR00119; CATRTPASE.
CC PROSITE: PS00154; ATPASE_E1_E2; 1.
CC Hydrolase; Calcium transport; Transmembrane; Phosphorylation;
CC Magnesium; ATP-binding; Alternative splicing.
CC KW DOMAIN 1 59 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 60 78 POTENTIAL.
CC FT TRANSMEM 79 89 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 90 110 POTENTIAL.
CC FT TRANSMEM 111 262 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 263 282 POTENTIAL.
CC FT TRANSMEM 283 300 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 301 318 POTENTIAL.
CC FT TRANSMEM 319 775 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 776 799 POTENTIAL.
CC FT TRANSMEM 800 840 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 841 863 POTENTIAL.
FT DOMAIN 864 898 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 899 917 POTENTIAL.
FT TRANSMEM 918 934 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 935 954 POTENTIAL.
FT DOMAIN 955 1003 CYTOPLASMIC (POTENTIAL).
FT MOD_RES 354 354 PHOSPHORYLATION (BY SIMILARITY).
FT BINDING 519 519 ATP (BY SIMILARITY).
FT VARSLIC 998 1003 ESF1K -> GMP15XPYDANGVIVAMLFFGVIFYSP
FT CONFLICT 481 481 T -> A (IN REF. 2).
FT CONFLICT 793 793 P -> Q (IN REF. 2).
SQ SEQUENCE 1003 AA; 110343 MM; 908A036A19FAF03E CRC64;

Query Match
Best Local Similarity 52.0%; Score 39.5; DB 1; Length 1003;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 2 GLN-YOIEHHL 11
Db 868 GLNFYQLSHLL 878

RESULT 7
MATIC_NEUCR STANDARD: PRT: 373 AA.
ID MATIC_NEUCR
AC Q10115;
DT 01-FEB-1996 (rel. 33, Created)
DT 01-FEB-1996 (rel. 33, Last sequence update)
DT 01-OCT-2000 (rel. 40, Last annotation update)
DE MATING TYPE PROTEIN A-2 (MT A-2) (UPPER CASE "A").
GN MTA-2.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_Taxid=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=74-OR23-1A;
RX MEDLINE=96204518; PubMed=8628238;
RA Ferreira A.V.B., Saude S., Glass N.L.;
RT "Transcriptional analysis of the mta1 idiomorph of Neurospora crassa
RT identifies two genes in addition to mta-1."
RT Mol. Gen. Genet. 250:767-774(1996).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: TO P. ANSERINA SMR1.
-----
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CC EMBL: M33876; AAC37477.1; -
CC KW Fertilization; Transcription regulation; Activator; DNA-binding;
CC Nuclear protein.
CC KW SEQUENCE 373 AA; 42878 MM; CFIPEB041009FC0 CRC64;

Query Match
Best Local Similarity 51.3%; Score 39; DB 1; Length 373;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGLNIOIEHHLFP 13
Db 192 GGRNHHVHTLHP 204

RESULT 8
VGIM_EBV

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ID VGLM_EBV STANDARD: PRT: 405 AA.
AC P03215;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE GLYCOPROTEIN M.
GN BBRP3.
OS Epstein-Barr virus (strain B95-8) (Human herpesvirus 4).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=10377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84270667; PubMed=6087149;
RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
RA Tuffnell P.S., Barrell B.G.;
RT "RNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RL Nature 310:207-211(1984).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEIN M.
CC -----
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CC -----
CC EMBL: V01555; CAA24825.1; -.
DR PIR: A03777; Q0BE35.
DR PIR: S33030; S33030.
DR InterPro: IPR000785; -.
DR Pfam: PF01528; Herpes_glycop. 1.
DR PRINTS: PR00333; HSVINTEGRMP.
KW Transmembrane; Glycoprotein; Late protein.
FT TRANSMEM 18 38 POTENTIAL.
FT TRANSMEM 77 97 POTENTIAL.
FT TRANSMEM 122 142 POTENTIAL.
FT TRANSMEM 150 170 POTENTIAL.
FT TRANSMEM 208 228 POTENTIAL.
FT TRANSMEM 246 266 POTENTIAL.
FT TRANSMEM 268 288 POTENTIAL.
FT TRANSMEM 300 320 POTENTIAL.
FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DOMAIN 367 377 SER/THR-RICH.
SQ SEQUENCE 405 AA; 45792 MW; 25A8A46B6CDC0AE1 CRC64;

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Query Match 51.3%; Score 39; DB 1; Length 405;
Best Local Similarity 60.0%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 4 NYOIEHHLP 13
   ||| |
Db 59 NYNLAHHLP 68

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RESULT 9
PCK1_SCHPO STANDARD: PRT: 988 AA.
AC P36582;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PROTEIN KINASE C-LIKE 1 (EC 2.7.1.-).
OS PCK1 OR SPAC22H10.01C OR SPAC17G8.14C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.

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OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93259141; PubMed=8491190;
RA Toda T., Shimanuki M., Yanagida M.;
RT "Two novel protein kinase C-related genes of fission yeast are
RT essential for cell viability and implicated in cell shape control.";
RL EMO J. 12:1987-1995(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (Feb-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN THE CONTROL OF THE CELL SHAPE. TARGET
CC OF THE INHIBITOR STAUSPORINE.
CC -1- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHOSBO-ESTER AND DAG
CC BINDING DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC -----
DR EMBL: D14337; BA03267.1; -.
DR EMBL: Z69730; CAA93602.1; -.
DR EMBL: Z69795; CAA93697.1; -.
DR PIR: S35362; S35362.
DR HSSP: O63450; 1A06.
DR InterPro: IPR000719; -.
DR InterPro: IPR000961; -.
DR InterPro: IPR002219; -.
DR InterPro: IPR002290; -.
DR Pfam: PF00130; DAG_PE-bind. 2.
DR Pfam: PF00069; pkinase. 1.
DR Pfam: PF00433; pkinase.C. 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE: PS50081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE: PS0107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE-ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Zinc;
KW Phorbol-ester binding; Duplication.
FT DOMAIN 414 461 PHORBOL-ESTER AND DAG BINDING (BY
FT DOMAIN 481 530 PHORBOL-ESTER AND DAG BINDING (BY
FT DOMAIN 664 923 PROTEIN KINASE.
FT NP_BIND 670 678 ATP (BY SIMILARITY).
FT BINDING 693 693 ATP (BY SIMILARITY).
FT ACT_SITE 789 789 BY SIMILARITY.
FT CONFLICT 27 35 AMVASTKNP -> SNGGDDGS (IN REF. 1).
SQ SEQUENCE 988 AA; 111783 MW; 0969BDEC1AB43C4E CRC64;

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Query Match 51.3%; Score 39; DB 1; Length 988;
Best Local Similarity 53.8%; Pred. No. 49;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
OY 1 GGLNYOIEHHLP 13
   ||| |
Db 473 GGLRYRIPRHREP 485

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RESULT 10
YLO5_YEAST STANDARD: PRT: 367 AA.
ID YLO5_YEAST
AC 006063;
DT 01-NOV-1997 (Rel. 35, Created)

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DT 01-NOV-1997 (rel. 35, Last sequence update)
DE 01-NOV-1997 (rel. 35, Last annotation update)
DE HYPOHETICAL 41.7 KDA PROTEIN IN SFPI-CTR3 INTERGENIC REGION.
GN YLR405W OR L8084.2.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxId=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=288C / AB972;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Pavello A., Fallon T., Gattung S., Greco T., Kirsten J.,
RA Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
RA Johnson D., Johnston L., Langston Y., Latreille P., Le T.,
RA Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D.,
RA Rifken L., Riles L., Tatch A., Trevasakis E., Vignati D.,
RA Wilcox L., Wohlman P., Vaudin M., Wilson R., Waterston R.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE UPF0034 (NIFR3/SM1) FAMILY.
CC -----
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CC -----
CC
CC DR EMBL: U19729; AAB82341.1; -.
CC DR SGD: S0004397; YLR405W.
CC DR InterPro: IPR001269; -.
CC DR Pfam: PF01207; UPF0034; 1.
CC DR PROSITE: PS01136; UPF0034; 1.
CC KM Hypothetical protein.
SQ SEQUENCE 367 AA; 41696 MM; 653DFCCF13EAB968 CRC64;

Query Match
Best Local Similarity 50.7%; Score 38.5; DB 1; Length 367;
Matches 7; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

OY 1 GGLNYOI-EHHLF 12
   |||:::||||
DB 287 GGLPFLAQHLY 299

RESULT 11
RS7_RICPR STANDARD; PRT; 160 AA.
ID P41081;
AC P41081;
DT 01-FEB-1995 (rel. 31, Created)
DT 01-FEB-1995 (rel. 31, Last sequence update)
DT 30-MAY-2000 (rel. 39, Last annotation update)
DE 30S RIBOSOMAL PROTEIN S7.
GN RPS6 OR RPL31.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiidae; Rickettsia.
OX NCBI_TaxId=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E;
RA Wood D.O.;
RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E;
RX MEDLINE=99039499; PubMed=9823893;
RA Anderson S.G.E.; Zomrodipour A.; Andersson J.O.;
RA Sichteritz-Ponten T.; Alsmark U.C.M.; Podowski R.M.; Neeslund A.K.;
RA Eriksson A.-S.; Winkler H.H.; Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of

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RT mitochondria.";
RL Nature 396:133-140(1998).
CC -1- FUNCTION: PROTEIN S7 BINDS SPECIFICALLY TO PART OF THE 3' END OF
CC 16S RIBOSOMAL RNA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
CC
CC DR EMBL: U02603; AAA18330.1; -.
CC DR EMBL: AJ235270; CAA14600.1; -.
CC DR HSSP: P22744; 1H05.
CC DR InterPro: IPR000235; -.
CC DR Pfam: PF00177; Ribosomal_S7; 1.
CC DR PROSITE: PS00052; RIBOSOMAL_S7; 1.
CC KM Ribosomal protein; rRNA-binding.
SQ SEQUENCE 160 AA; 18309 MM; 5C66702A37F41761 CRC64;

Query Match
Best Local Similarity 50.0%; Score 38; DB 1; Length 160;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGLNYOIEHHL 11
   ||||:|
DB 81 GCANYGVPTHV 91

RESULT 12
ATP6_MAIZE STANDARD; PRT; 291 AA.
ID ATP6_MAIZE
AC P07925;
DT 01-AUG-1988 (rel. 08, Created)
DT 01-AUG-1988 (rel. 08, Last sequence update)
DT 01-NOV-1997 (rel. 35, Last annotation update)
DE ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).
GN ATP6.
OS Zea mays (Maize).
OS Mitochondrion.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; PAC clade; Panicoideae;
OC Andropogoneae; Zea.
OX NCBI_TaxId=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA Dewey R.E.; Levings C.S. III, Timothy D.H.;
RT "Nucleotide sequence of ATPase subunit 6 gene of maize mitochondria.";
RL Plant Physiol. 79:914-919(1985).
CC -1- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A
CC DIRECT ROLE IN THE TRANSLLOCATION OF PROTONS ACROSS THE MEMBRANE.
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.
CC -----
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CC -----
CC
CC DR EMBL: M16223; AAA70270.1; -.
CC DR PIR: JN0042; Pw2M6M.
CC DR Matzdb: 69201; -.

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DR Mendel: 11435; 2EAmA.atp6.1.
DR InterPro: IPR000568; -.
DR Pfam: PF00119; ATP-synt_A; 1.
DR PRINTS: PR00123; ATPASEA.
DR PROSITE: PS00449; ATPASE_A; 1.
KM Hydrogen ion transport: CE(0); Mitochondrion; Transmembrane.
SQ SEQUENCE 291 AA; 31758 MW; 97749E9C3AC70477 CRC64;

Query Match 50.0%; Score 38; DB 1; Length 291;
Best Local Similarity 46.2%; Pred. No. 21;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGLNQLIEHLFP 13
111: :111
DB 101 GGLSGNVKHKFFP 113

RESULT 13
ID YH60_MYCTU STANDARD; PRT; 502 AA.
AC 006795;

DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE HYPOThETICAL 54.1 KDA PROTEIN RV1760.
GN RV1760 OR MTCY28.26.

OS Mycobacteria tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;

RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;

RA MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C., Harris D.,

RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holtroyd S.,
RA Harnaby T., Jagsels K., Krogh A., McLean J., Moule S., Murphy L.,

RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squires R., Stulson J.E.,

RA Taylor K., Whitehead S., Barrell B.G.;
RT Deciphering the biology of Mycobacterium tuberculosis from the

RT complete genome sequence."
RL Nature 393:537-544(1998).

CC -1- SIMILARITY: BELONGS TO THE UPF0089 FAMILY.

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CC EMBL: Z95890; CAB09323.1; -.
DR Tuberculin: RV1760; -.

KM Hypothetical protein.
SQ SEQUENCE 502 AA; 54092 MW; 833B9D3F900A43F2 CRC64;

Query Match 50.0%; Score 38; DB 1; Length 502;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 NYQLEHHL 11
1:11111
DB 112 NFQIRHHL 119

RESULT 14
AMPN_LACHE

ID AMPN_LACHE STANDARD; PRT; 844 AA.
AC Q10730;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE AMINOPEPTIDASE N (EC:3.4.11.2) (LYSL AMINOPEPTIDASE) (LYS-AP)
DE (ALANINE AMINOPEPTIDASE).
GN PEPN.

OS Lactobacillus helveticus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
OC Lactobacillus.

OX NCBI_TaxID=1587;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=CNZ 32;

RX MEDLINE=95212935; PubMed=7698673;
RA Christensen J.E., Lin D.-L., Palva A., Steele J.L.;

RT "Sequence analysis, distribution and expression of an aminopeptidase
RT N-encoding gene from Lactobacillus helveticus CNZ32.";

RL Gene 155:89-93(1995).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=53/77;

RX MEDLINE=95154667; PubMed=7851738;
RA Varmanen P., Vesanto E., Steele J.L., Palva A.;

RT "Characterization and expression of the pepN gene encoding a general
RT aminopeptidase from Lactobacillus helveticus."

RL FEMS Microbiol. Lett. 124:315-320(1994)
CC -1- FUNCTION: AMINOPEPTIDASE N IS INVOLVED IN THE DEGRADATION OF

CC INTRACELLULAR PEPTIDES GENERATED BY PROTEIN BREAKDOWN DURING
CC NORMAL GROWTH AS WELL AS IN RESPONSE TO NUTRIENT STARVATION

CC (BY SIMILARITY).
CC -1- COFACTOR: BINDS ONE ZINC ION.

CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M1 (ZINC METALLOPROTEASES);
CC ALSO KNOWN AS THE PEPN SUBFAMILY.

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CC or send an email to license@isb-sib.ch).

CC EMBL: U08224; AAA81951.1; -.
DR EMBL: Z30323; CAAB2978.1; -.

DR MEROPS: M01.002; -.
DR InterPro: IPR000130; -.

DR InterPro: IPR001930; -.
DR Pfam: PF01433; Peptidase_M1; 1.

DR PRINTS: PR00756; ALADIPASE.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.

KM Hydrolyase: Metalloprotease; Aminopeptidase; zinc.
KW METAL 289

FT ACT_SITE 290 290 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 293 293 ZINC (CATALYTIC) (BY SIMILARITY).

FT METAL 312 312 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 376 376 PROTON DONOR (POTENTIAL).

FT VARIANT 39 39 F -> I (IN REF. 2).
FT VARIANT 44 44 L -> F (IN REF. 2).

FT VARIANT 342 342 S -> A (IN REF. 2).
FT VARIANT 455 455 K -> R (IN REF. 2).

FT VARIANT 496 496 S -> N (IN REF. 2).
FT VARIANT 527 527 H -> L (IN REF. 2).

SQ SEQUENCE 844 AA; 95837 MW; 1EASD6AC69410F4 CRC64;

Query Match 50.0%; Score 38; DB 1; Length 844;
Best Local Similarity 54.5%; Pred. No. 63;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 GUNYQIEHHLF 12
 || | : || |
 DB 398 GLKYFDHHRF 408

RESULT 15
 UL70_MCMVS STANDARD: PRT; 964 AA.
 ID UL70_MCMVS
 AC 069153;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE HELICASE/PRIMASE COMPLEX PROTEIN (PROBABLE DNA REPLICATION PROTEIN
 DE UL70).
 GN UL70.
 OS Murine cytomegalovirus (strain Smith).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Murinegaloivirus.
 OX NCBI_TaxID=10367;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96082764; PubMed=7483291;
 RA Messerle M., Rapp M., Lucin P., Koszlinowski U.H.;
 RT "Characterization of a conserved gene block in the murine
 cytomagalovirus genome."
 RL Virus Genes 10:73-80(1995).
 CC -1- FUNCTION: INVOLVED IN DNA REPLICATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL52,
 CC EBV-1 7, EBV BSLE1, HSV-1 56, VZV 6, HCMV AND MCMV UL70.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: L07319; AAA96665.1; -
 CC Helicase; DNA replication.
 KW SEQUENCE 964 AA; 109704 MW; 70605300E1D85864 CRC64;
 SO

Query Match 50.0%; Score 38; DB 1; Length 964;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 EHHLP 13
 |||||
 DB 26 EHHLP 31

Search completed: August 9, 2001, 20:36:52
 Job time: 701 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 9, 2001, 20:36:18 ; Search time 87.05 Seconds
(without alignments)
19.758 Million cell updates/sec

Title: US-09-367-013b-2_COPY_390_402
Perfect score: 76
Sequence: 1 GGLNYQIEHHLFP 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_16:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_unclassified:*
13: sp_virtebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76	100.0	347	2 Q9FC35	Q9FC35 streptomyc
2	76	100.0	350	2 Q9F2M3	Q9F2M3 streptomyc
3	76	100.0	357	3 Q9HDF4	Q9HDF4 mortierella
4	76	100.0	443	5 Q61388	Q61388 caenorhabdi
5	76	100.0	443	5 Q23221	Q23221 caenorhabdi
6	76	100.0	447	5 Q9XTB7	Q9XTB7 caenorhabdi
7	76	100.0	457	3 Q9UVV3	Q9UVV3 mortierella
8	76	100.0	457	3 Q9UUV3	Q9UUV3 mortierella
9	76	100.0	457	3 Q9HEX4	Q9HEX4 mortierella
10	76	100.0	457	3 Q9HEV1	Q9HEV1 mortierella
11	72	94.7	428	5 Q9N9B5	Q9N9B5 leishmania
12	71	93.4	345	2 Q9XBW4	Q9XBW4 streptomyc
13	71	93.4	419	10 Q9SMO9	Q9SMO9 euglena gra
14	67	88.2	520	10 Q9LEM9	Q9LEM9 ceratodon p
15	67	88.2	525	10 Q9ZNM2	Q9ZNM2 physcomitri
16	66	86.8	448	10 Q04353	Q04353 borago offi
17	66	86.8	448	10 Q9SAU5	Q9SAU5 borago offi
18	65	85.5	469	10 Q9ZTU8	Q9ZTU8 triticum ae
19	64	84.2	311	4 Q9Y3X4	Q9Y3X4 homo sapien

20	64	84.2	368	2 Q54795	Q54795 spirulina p
21	64	84.2	422	4 Q9H3G3	Q9H3G3 homo sapien
22	64	84.2	444	4 Q9NYX1	Q9NYX1 homo sapien
23	64	84.2	444	4 Q9NRP8	Q9NRP8 homo sapien
24	64	84.2	444	4 Q60427	Q60427 homo sapien
25	64	84.2	444	4 Q95864	Q95864 homo sapien
26	64	84.2	444	11 Q92122	Q92122 ratcus norv
27	64	84.2	444	11 Q9ZOR9	Q9ZOR9 mus musculu
28	64	84.2	444	13 Q9DEX7	Q9DEX7 brachydanio
29	64	84.2	444	13 Q9DEX6	Q9DEX6 cyprinus ca
30	64	84.2	445	4 Q9Y500	Q9Y500 homo sapien
31	64	84.2	446	10 Q9ZRT9	Q9ZRT9 arabisidops
32	64	84.2	446	10 Q9FER8	Q9FER8 borago offi
33	64	84.2	449	10 Q82348	Q82348 arabisidops
34	64	84.2	449	10 Q9ZRP8	Q9ZRP8 brassica na
35	64	84.2	449	10 Q9ZRP7	Q9ZRP7 arabisidops
36	64	84.2	449	11 Q9ZUE7	Q9ZUE7 mus musculu
37	64	84.2	458	10 Q43469	Q43469 helianthus
38	62	82.9	446	10 Q9ZTY9	Q9ZTY9 ricinus com
39	63	81.6	483	10 Q9LENO	Q9LENO ceratodon p
40	58	76.3	446	3 Q74212	Q74212 mortierella
41	58	76.3	447	11 Q9EPV4	Q9EPV4 ratcus norv
42	58	76.3	523	3 Q9HDE8	Q9HDE8 mucor rouxi
43	57	75.0	370	2 Q9HUS5	Q9HUS5 pseudomonas
44	57	75.0	464	5 Q9Y1W0	Q9Y1W0 dictyostell
45	54	71.1	361	2 Q85776	Q85776 rhizobium 1

ALIGNMENTS

RESULT 1
ID Q9FC35 PRELIMINARY: PRT: 347 AA.
AC Q9FC35;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PUTATIVE DELTA FATTY ACID DESATURASE.
GN SCAG1.14C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Brown S.P.;
RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denaparte D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmid and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996);
DR EMBL, AL391039; CAC01546.1;--
SQ SEQUENCE 347 AA; 37990 MW; 201E2D716CB46419 CRC64;

Query Match 100.0%; Score 76; DB 2; Length 347;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGLNYQIEHHLFP 13
|||||

Db 283 GGLNVOIEHHLP 295

RESULT 2

09F2M3

ID 09F2M3 PRELIMINARY: PRT: 350 AA.

AC 09F2M3: 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

OS PUTATIVE FATTY ACID DESATURASE.

GN SCH63.05C.

OS Streptomyces coelicolor.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=1902;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-A3(2);

RA Oliver K., Harris D.;

DT Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-A3(2);

RA Cereno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;

DT Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN-A3(2);

RA MEDLINE-97000351; PubMed-8843436;

RA Redenbach M., Kleser H.M., Denapate D., Eichner A., Cullum J.,

RA Kinash H., Hopwood D.A.;

RT "A set of ordered cosmids and a detailed genetic and physical map for

the 8 Mb streptomyces coelicolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

DR EMBL: AL442629; CAC10296.1; -

DL

SO SEQUENCE 350 AA; 38678 MW; 240C0BA1F428E5 CRC64;

Query Match 100.0%; Score 76; DB 2; Length 350;

Best Local Similarity 100.0%; Pred. No. 2.3e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGLNVOIEHHLP 13

DB 286 GGLNVOIEHHLP 298

RESULT 3

09HDF4

ID 09HDF4 PRELIMINARY: PRT: 357 AA.

AC 09HDF4: 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

OS DELTA 6-FATTY ACID DESATURASE (FRAGMENT).

OC Mortierella alpina.

OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae;

OC Mortierella.

OX NCBI_TaxID=64518;

RN [1]

RP SEQUENCE FROM N.A.

RA Xing L., Li M., Liu L., Hu G.;

DT "Cloning and sequence analysis of the conserved region of delta 6-

fatty acid desaturase gene from Mortierella alpina.";

Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Xing L., Li M., Liu L., Hu G., Zhang L.;

DT "Cloning and sequence analysis of the conserved region of delta 6-

fatty acid desaturase gene from Mortierella alpina.";

Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.

DR

SO EMBL: AF307942; AAG45094.1; -

DR EMBL: AF307941; AAG45093.1; -

FT NON_TER 1

FT NON_TER 357

SO SEQUENCE 357 AA; 40796 MW; C8D9CE1283BB16B8 CRC64;

Query Match 100.0%; Score 76; DB 3; Length 357;

Best Local Similarity 100.0%; Pred. No. 2.3e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGLNVOIEHHLP 13

DB 345 GGLNVOIEHHLP 357

RESULT 4

061388

ID 061388 PRELIMINARY: PRT: 443 AA.

AC 061388: 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)

DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

OS Caenorhabditis elegans.

OC Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE-9768723; PubMed-9108131;

RA Sayanova O., Smith M.A., Lapinskas P., Stobart A.K., Dobson G.,

RA Christie W.W., Shewry P.R., Napier J.A.;

RT "Expression of a borage desaturase cDNA containing an N-terminal

cytochrome b5 domain results in the accumulation of high levels of

delta6-desaturated fatty acids in transgenic tobacco.";

Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).

DL

SO SEQUENCE 443 AA; 51740 MW; 9513CA7C5A7E9A06 CRC64;

Query Match 100.0%; Score 76; DB 5; Length 443;

Best Local Similarity 100.0%; Pred. No. 3e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGLNVOIEHHLP 13

DB 378 GGLNVOIEHHLP 390

RESULT 5

023221

ID 023221 PRELIMINARY: PRT: 443 AA.

AC 023221: 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

OS W08D2.4 PROTEIN.

OC Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

```

RN [1]
RP SEQUENCE FROM N.A.
RA Swinburne J., Ainscough R.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Swinburne J.;
RX MEDLINE=99069613; PubMed=9851916;
RT "Genome sequence of the nematode C.elegans: A platform for
  investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; 270271; CA94233.2; -.
DR InterPro; IPR000566; -.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
SQ SEQUENCE 443 AA; 51772 MW; 9513D611ECB99A06 CRC64;

Query Match 100.0%; Score 76; DB 5; Length 443;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGLNYQIEHHLFP 13
Db 378 GGLNYQIEHHLFP 390

RESULT 6
Q9XBT7 PRELIMINARY; PRT; 447 AA.
ID Q9XBT7;
AC Q9XBT7;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE DELTA5-FATTY ACID DESATURASE.
GN FAT-4 OR DES-5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99117288; PubMed=9917342;
RA Watts J.B., Browne J.;
RT "Isolation and characterisation of a delta5-fatty acid desaturase from
  Caenorhabditis elegans.";
RL Arch. Biochem. Biophys. 362:175-182(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99059458; PubMed=9845325;
RA Michelson L.V., Napier J.A., Lewis M., Griffiths G., Lazarus C.M.,
  Stobart A.K.;
RT "Functional identification of a fatty acid delta5 desaturase gene from
  Caenorhabditis elegans.";
RL FEMS Lett. 439:215-218(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Swinburne J.;
RN Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
  investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AF114440; AAD13294.1; -.
DR EMBL; AF078796; AAC95143.1; -.
DR EMBL; Z81122; CAB61031.1; -.
SQ SEQUENCE 447 AA; 52348 MW; D7E09CE0E2975015 CRC64;

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Query Match 100.0%; Score 76; DB 5; Length 447;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGLNYQIEHHLFP 13
Db 379 GGLNYQIEHHLFP 391

RESULT 7
Q9UVV3 PRELIMINARY; PRT; 457 AA.
ID Q9UVV3;
AC Q9UVV3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE DELTA-6 FATTY ACID DESATURASE.
OS Mortierella alpina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae;
OC Mortierella.
OX NCBI_TaxID=64518;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC32221;
RX MEDLINE=99406036; PubMed=10478922;
RA Huang Y.S., Chaudhary S., Thurmond J.M., Bobik E.G., Jr., Yuan L.,
  Chan G.M., Kirchner S.J., Mukerji P., Knutzen D.S.;
RT "Cloning of delta12- and delta6-desaturases from Mortierella alpina
  and recombinant production of gamma-linolenic acid in Saccharomyces
  cerevisiae.";
RL Lipids 34:649-659(1999).
CC -i SIMILARITY: TO CYTOCHROME B5 DOMAIN.

Query Match 100.0%; Score 76; DB 3; Length 457;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGLNYQIEHHLFP 13
Db 390 GGLNYQIEHHLFP 402

RESULT 8
Q9UVV3 PRELIMINARY; PRT; 457 AA.
ID Q9UVV3;
AC Q9UVV3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE DELTA-6 FATTY ACID DESATURASE.
OS Mortierella alpina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae;
OC Mortierella.
OX NCBI_TaxID=64518;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC32221;
RX MEDLINE=99406036; PubMed=10478922;
RA Huang Y.S., Chaudhary S., Thurmond J.M., Bobik E.G., Jr., Yuan L.,
  Chan G.M., Kirchner S.J., Mukerji P., Knutzen D.S.;
RT "Cloning of delta12- and delta6-desaturases from Mortierella alpina
  and recombinant production of gamma-linolenic acid in Saccharomyces
  cerevisiae.";
RL Lipids 34:649-659(1999).
CC -i SIMILARITY: TO CYTOCHROME B5 DOMAIN.

```

DR EMBL: AF110510; AAF08685.1; -
DR HSSP: P04166; 1BSM.
DR InterPro: IPR001199; -
DR Pfam: PF00173; heme_1; 1.
DR PROSITE: PS00191; CYTOCHROME_B5_1; UNKNOWN_1.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 457 AA; 51837 MW; D90169E86911450A CRC64;

Query Match 100.0%; Score 76; DB 3; Length 457;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGLNYOIEHHLP 13
|||||
DB 390 GGLNYOIEHHLP 402

RESULT 9
O9HEY4 PRELIMINARY; PRT; 457 AA.
AC O9HEY4:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE DELTA6-FATTY ACID DESATURASE.
OS Mortierella isabellina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae;
OC Mortierella.
OX NCBI_TaxID=91625;
RN [1]
RP SEQUENCE FROM N.A.
RA Ming-Chun L., Li L., Guo-Wu H., Li Z., Lai-Jun X.;
RT "Cloning and sequencing analysis of delta6-fatty acid desaturase gene
from Mortierella isabellina";
RL Junwu Xilong 0:0-0(2001).
DR EMBL: AF306634; AAG38104.1; -
SQ SEQUENCE 457 AA; 51772 MW; 868E7EB21172D5AF CRC64;

Query Match 100.0%; Score 76; DB 3; Length 457;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGLNYOIEHHLP 13
|||||
DB 390 GGLNYOIEHHLP 402

RESULT 10
O9HEY1 PRELIMINARY; PRT; 457 AA.
AC O9HEY1:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE DELTA6-FATTY ACID DESATURASE.
OS Mortierella alpina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae;
OC Mortierella.
OX NCBI_TaxID=64518;
RN [1]
RP SEQUENCE FROM N.A.
RA Xing L., Li M., Liu L., Hu G., Zhang L.;
RT "Expression of Mortierella alpina delta 6-fatty acid desaturase gene
in Saccharomyces cerevisiae";
RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF307940; AAG45092.1; -
SQ SEQUENCE 457 AA; 51885 MW; 4B0ACODD15D1DA1 CRC64;

Query Match 100.0%; Score 76; DB 3; Length 457;

Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGLNYOIEHHLP 13
|||||
DB 390 GGLNYOIEHHLP 402

RESULT 11
O9NB5 PRELIMINARY; PRT; 428 AA.
AC O9NB5:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE POSSIBLE FATTY ACID DESATURASE.
GN P1408.11.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FRIEDLIN;
RA Bothé G., Pohl T., Ivens A.C., Quail M., Rajandream M.A.,
RA Barrell B.G.;
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-FRIEDLIN;
RX MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome";
RL "Genome Res. 8:135-145(1998)."
DR EMBL: AL358652; CAB94021.1; -
SQ SEQUENCE 428 AA; 49418 MW; D6CEFD70EDD8907 CRC64;

Query Match 94.7%; Score 72; DB 5; Length 428;
Best Local Similarity 92.3%; Pred. No. 0.00014;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGLNYOIEHHLP 13
|||||
DB 361 GGLNYOIEHHLP 373

RESULT 12
O9XBW4 PRELIMINARY; PRT; 345 AA.
AC O9XBW4:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE PUTATIVE DELTA FATTY ACID DESATURASE.
GN SCH35.42C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Oliver K., Harris D.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome";
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
RN [3]

RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kleser H.M., Denapate D., Eichner A., Cullum J.,
RA Kinastri H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL M01. Microbiol. 21:77-96(1996).
DR EMBL: AL078610; CAB4385.1; -;
SQ SEQUENCE 345 AA; 38022 MW; 1C938614F662DCA CRC64;

Query Match 93.4%; Score 71; DB 2; Length 345;
Best Local Similarity 92.3%; Pred. No. 0.00017;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGLNYQIEHHLFP 13
DB 278 GGLNROIEHHLFP 290

RESULT 13

Q9SMO9 PRELIMINARY; PRT; 419 AA.
ID Q9SMO9;
AC Q9SMO9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE DELTA8 FATTY ACID DESATURASE.
GN EFD1.
OS Euglena gracilis.
OC Eukaryota; Euklenozoa; Euglenida; Euglenales; Euglena.
OX NCBI_TaxID=3039;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=Z;
RX MEDLINE=99262077; PubMed=10328826;
RA Wallis J.G., Browne J.;
RT "The Delta8-desaturase of Euglena gracilis: an alternate pathway for
the synthesis of 20-carbon polyunsaturated fatty acids.";
RL Arch. Biochem. Biophys. 365:307-316(1999).
DR EMBL: AF139720; AAD45877.1; -;
DR InterPro: IPR001199; -;
DR PROSITE: PSS0255; CYTOCHROME_B5_2; 1.

SQ SEQUENCE 419 AA; 48457 MW; C2D8EDD092F27EB2 CRC64;

Query Match 93.4%; Score 71; DB 10; Length 419;
Best Local Similarity 92.3%; Pred. No. 0.00021;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGLNYQIEHHLFP 13
DB 350 GGLNYQIEHHLFP 362

RESULT 14

Q9LEM9 PRELIMINARY; PRT; 520 AA.
ID Q9LEM9;
AC Q9LEM9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE DELTA 6-FATY ACID DESATURASE.
OS Ceratodon purpureus (Moss).
OC Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida;
OC Dicranidae; Dicranales; Ditrichaceae; Ceratodon.
OX NCBI_TaxID=3225;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=WT3; TISSUE=PROTONEMATA;
RX MEDLINE=20307617; PubMed=10848999;
RA Sperling P., Lee M., Girke T., Zaehrlinger U., Stymer S., Heinz E.;

RT "A bifunctional delta 6-fatty acyl acetylase/desaturase from the
RT moss Ceratodon purpureus. A new member of the cytochrome b5
RT superfamily.";
RL Eur. J. Biochem. 267:3801-3811(2000).
DR EMBL: AJ250735; CAB94993.1; -;
DR InterPro: IPR001199; -;
DR Pfam: PF00173; heme_1; 1.
DR PROSITE: PSS0255; CYTOCHROME_B5_2; 1.

SQ SEQUENCE 520 AA; 59160 MW; 5A9332EECC153439 CRC64;

Query Match 88.2%; Score 67; DB 10; Length 520;
Best Local Similarity 92.3%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGLNYQIEHHLFP 13
DB 452 GGLNROIEHHLFP 464

RESULT 15

Q9ZNM2 PRELIMINARY; PRT; 525 AA.
ID Q9ZNM2;
AC Q9ZNM2;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE DELTA6-ACYL-LIPID DESATURASE.
GN DES6.
OS Physcomitrella patens (Moss).
OC Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida;
OC Funariidae; Funariales; Funariaceae; Physcomitrella.
OX NCBI_TaxID=3218;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=HEBW. B. S. G.;
RX MEDLINE=98416756; PubMed=9744093;
RA Girke T., Schmidt H., Zaehrlinger U., Reekl R., Heinz E.;
RT "Identification of a novel delta 6-acyl-group desaturase by targeted
gene disruption in Physcomitrella patens.";
RL Plant J. 15:39-48(1998).
CC -1- SIMILARITY: TO CYTOCHROME B5 DOMAIN.
DR EMBL: AJ222981; CAA11033.1; -;
DR EMBL: AJ222980; CAA11032.1; -;
DR HSSP: P04166; IBSM.
DR InterPro: IPR001199; -;
DR Pfam: PF00173; heme_1; 1.
DR PROSITE: PSS0255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 525 AA; 59369 MW; 530F158B0C97C83F CRC64;

Query Match 88.2%; Score 67; DB 10; Length 525;
Best Local Similarity 92.3%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGLNYQIEHHLFP 13
DB 457 GGLNROIEHHLFP 469

Search completed: August 9, 2001, 20:36:18
Job time: 717 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 9, 2001, 20:36:16 ; Search time 87.05 Seconds
(without alignments)
7.599 Million cell updates/sec

Title: US-09-367-013b-2_COPY_172_176

Perfect score: 32

Sequence: 1 HDPLH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP mhc: *
8: SP organelle: *
9: SP phage: *
10: SP plant: *
11: SP rodent: *
12: SP unclassified: *
13: SP vertebrate: *
14: SP virus: *

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	357	3 Q9HDF4	Q9HDF4 mortierella
2	32	100.0	457	3 Q9UVY3	Q9UVY3 mortierella
3	32	100.0	457	3 Q9UVV3	Q9UVV3 mortierella
4	32	100.0	457	3 Q9HEX4	Q9HEX4 mortierella
5	32	100.0	457	3 Q9HEY1	Q9HEY1 mortierella
6	32	100.0	483	10 Q9LENO	Q9LENO ceratodon p
7	32	100.0	520	10 Q9LEME9	Q9LEME9 ceratodon p
8	32	100.0	565	10 Q9ZNMW2	Q9ZNMW2 physcomit
9	32	100.0	582	3 P94896	P94896 oenococcus
10	32	100.0	582	3 Q04089	Q04089 saccharomyc
11	32	100.0	609	4 Q9NVN4	Q9NVN4 homo sapien
12	32	100.0	717	10 Q9JUL4	Q9JUL4 arabidopsis
13	32	100.0	917	11 Q54810	Q54810 mus musculu
14	32	100.0	917	11 Q9QZD4	Q9QZD4 mus musculu
15	32	100.0	918	4 Q9UGA1	Q9UGA1 homo sapien
16	32	100.0	1196	4 Q94834	Q94834 homo sapien
17	30	93.8	254	14 Q90199	Q90199 hz-1 insect
18	30	93.8	414	2 Q9X404	Q9X404 methylosulf
19	30	93.8	469	8 Q9MJ62	Q9MJ62 physarum po

20	30	93.8	530	10 Q9FPN6	Q9FPN6 oryza sativ
21	30	93.8	623	2 Q9KB08	Q9KB08 bacillus ha
22	30	93.8	628	5 Q18005	Q18005 caenorhabd1
23	30	93.8	743	3 P87122	P87122 schizosach
24	30	93.8	764	10 P93567	P93567 solanum tub
25	30	93.8	949	5 Q77386	Q77386 plasmodium
26	29	90.6	236	5 Q9XW27	Q9XW27 caenorhabd1
27	29	90.6	255	1 Q9UWS2	Q9UWS2 sulfolobus
28	29	90.6	331	5 Q9VLV0	Q9VLV0 drosophila
29	29	90.6	336	1 Q28306	Q28306 archaeoglob
30	29	90.6	339	5 Q9V816	Q9V816 drosophila
31	29	90.6	384	2 Q9KPM7	Q9KPM7 vibrio chol
32	29	90.6	403	10 Q9LLP3	Q9LLP3 oryza sativ
33	29	90.6	560	5 Q9U5A7	Q9U5A7 schistosoma
34	29	90.6	668	10 Q9SH55	Q9SH55 arabidopsis
35	29	90.6	691	11 Q35804	Q35804 rattus norv
36	29	90.6	941	5 Q17352	Q17352 caenorhabd1
37	29	90.6	1766	5 Q9V591	Q9V591 drosophila
38	28	87.5	108	9 Q9F2X7	Q9F2X7 bacteriophage
39	28	87.5	172	1 Q9HQ06	Q9HQ06 halobacteri
40	28	87.5	188	10 Q65127	Q65127 ranunculus
41	28	87.5	200	11 Q60464	Q60464 cricetus
42	28	87.5	204	3 Q9U009	Q9U009 schizosach
43	28	87.5	241	5 Q9GTN3	Q9GTN3 drosophila
44	28	87.5	249	5 Q9GTN4	Q9GTN4 drosophila
45	28	87.5	253	5 Q9V421	Q9V421 drosophila

ALIGNMENTS

RESULT 1
Q9HDF4 PRELIMINARY: PRT: 357 AA.
ID Q9HDF4
AC Q9HDF4
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE DELTA 6-FATTY ACID DESATURASE (FRAGMENT).
OS Mortierella alpina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae;
OC Mortierella.
OX NCBI_Taxid=64518;
RN [1]
RP SEQUENCE FROM N.A.
RA Xing L., Li M., Liu L., Hu G., Zhang L.;
RT "Cloning and sequence analysis of the conserved region of delta 6-
RT fatty acid desaturase gene from Mortierella alpina."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF307942; AAC45094.1; -.
DR EMBL: AF307941; AAC45093.1; -.
FT NON_TER
FT 357
SQ SEQUENCE 357 AA; 40796 MW; C8D9CE1283B16B8 CRC64;

Query Match 100.0%; Score 32; DB 3; Length 357;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDPLH 5
|||||
Db 127 HDPLH 131

RESULT 2
Q9UVY3

ID Q9UVY3 PRELIMINARY; PRT; 457 AA.
AC Q9UVY3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, last annotation update)
OC DELTA-6 FATTY ACID DESATURASE.
OS Mortierella alpina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae;
OC Mortierella.
OX NCBI_TaxID=64518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-IS-4;
RX MEDLINE-20035749; PubMed-10570972;
RA Sakuradani E., Kobayashi M., Shimizu S.;
RT "Delta 6-Fatty acid desaturase from an arachidonic acid-producing
RT Mortierella fungus. Gene cloning and its heterologous expression in a
RT fungus, Aspergillus.";
RL Gene 238:445-453(1999).
CC -1- SIMILARITY: TO CYTOCHROME B5 DOMAIN.
DR EMBL: AB020032; BAA85588.1; -.
DR HSSP: P04166; 1BSM.
DR InterPro: IPR001199; -.
DR Pfam: PF00173; heme_1; 1.
DR PROSITE: PS00191; CYTOCHROME_B5_1; UNKNOWN_1.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 457 AA: 51816 MW; 5C4B3D7312439543 CRC64;

Query Match 100.0%; Score 32; DB 3; Length 457;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDEFLH 5
Db 172 HDFLH 176

RESULT 3
Q9UVY3 PRELIMINARY; PRT; 457 AA.
AC Q9UVY3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, last annotation update)
OC DELTA-6 FATTY ACID DESATURASE.
OS Mortierella alpina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae;
OC Mortierella.
OX NCBI_TaxID=64518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC32221;
RX MEDLINE-99406036; PubMed-10478922;
RA Huang Y.S., Chaudhary S., Thurmond J.M., Bobik E.G. Jr., Yuan L.,
RA Chan G.M., Kitchner S.J., Mukerji P., Knutson D.S.;
RT "Cloning of delta12- and delta6-desaturases from Mortierella alpina
RT and recombinant production of gamma-linolenic acid in Saccharomyces
RT cerevisiae.";
RL Lipids 34:649-659(1999).
CC -1- SIMILARITY: TO CYTOCHROME B5 DOMAIN.
DR EMBL: AF110510; AAF08685.1; -.
DR HSSP: P04166; 1BSM.
DR InterPro: IPR001199; -.
DR Pfam: PF00173; heme_1; 1.
DR PROSITE: PS00191; CYTOCHROME_B5_1; UNKNOWN_1.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 457 AA: 51837 MW; D90169E86911450A CRC64;

Query Match 100.0%; Score 32; DB 3; Length 457;

Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDEFLH 5
Db 172 HDFLH 176

RESULT 4
Q9HEY4 PRELIMINARY; PRT; 457 AA.
AC Q9HEY4;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, last annotation update)
OC DELTA-6 FATTY ACID DESATURASE.
OS Mortierella isabellina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae;
OC Mortierella.
OX NCBI_TaxID=91625;
RN [1]
RP SEQUENCE FROM N.A.
RA Ming-Chun L., Li D., Guo-Wu H., Li Z., Lai-Jun X.;
RT "Cloning and sequencing analysis of delta6-fatty acid desaturase gene
RT from Mortierella isabellina.";
RL Junwu Xitong 0:0-0(2001).
DR EMBL: AF306634; AAG38104.1; -.
SQ SEQUENCE 457 AA: 51772 MW; 868E7EB21172D5AF CRC64;

Query Match 100.0%; Score 32; DB 3; Length 457;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDEFLH 5
Db 172 HDFLH 176

RESULT 5
Q9HEY1 PRELIMINARY; PRT; 457 AA.
AC Q9HEY1;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, last annotation update)
OC DELTA-6 FATTY ACID DESATURASE.
OS Mortierella alpina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae;
OC Mortierella.
OX NCBI_TaxID=64518;
RN [1]
RP SEQUENCE FROM N.A.
RA Xing L., Li M., Liu L., Hu G., Zhang L.;
RT "Expression of Mortierella alpina delta 6-fatty acid desaturase gene
RT in Saccharomyces cerevisiae.";
RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF307940; AAG45092.1; -.
SQ SEQUENCE 457 AA: 51885 MW; 4B0ACODD15D19DA1 CRC64;

Query Match 100.0%; Score 32; DB 3; Length 457;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDEFLH 5
Db 172 HDFLH 176

RESULT 6
Q9LENO PRELIMINARY; PRT; 483 AA.

AC 09LENO; PRELIMINARY; PRT; 520 AA.
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE DELTA 6-FATTY ACETYLENASE.
 OS Ceratodon purpureus (Moss).
 OC Eukaryota; Viridiplantae; Embryophyta; Bryopsida;
 OC Eukaryota; Viridiplantae; Dicotyledinales; Ceratodon.
 NCBI_TaxID=3225;
 RN NCB1_TaxID=3225;
 RP SEQUENCE FROM N.A.
 RC STRAIN=WT3; TISSUE=PROTONEMATA;
 RX MEDLINE=20307617; PubMed=10848999;
 RA Sperling P., Lee M., Girke T., Zaehring U., Szyme S., Heinz E.;
 RT "A bifunctional delta 6-fatty acyl acetylenase/desaturase from the
 RT moss Ceratodon purpureus. A new member of the cytochrome b5
 RT superfamily.";
 RL Eur. J. Biochem. 267:3801-3811(2000).
 DR EMBL; AJ250734; CAB94992.1; -;
 DR InterPro: IPR001199; -;
 DR Pfam: PF00173; heme_1; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 SQ SEQUENCE 483 AA; 54857 MW; C451D042169AB1C2 CRC64;

Query Match 100.0%; Score 32; DB 10; Length 483;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDELH 5
 Db 212 HDELH 216

RESULT 7
 ID 09LEM9 PRELIMINARY; PRT; 520 AA.
 AC 09LEM9;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE DELTA 6-FATTY ACID DESATURASE.
 OS Ceratodon purpureus (Moss).
 OC Eukaryota; Viridiplantae; Embryophyta; Bryopsida;
 OC Eukaryota; Viridiplantae; Dicotyledinales; Ceratodon.
 NCBI_TaxID=3225;
 RN NCB1_TaxID=3225;
 RP SEQUENCE FROM N.A.
 RC STRAIN=WT3; TISSUE=PROTONEMATA;
 RX MEDLINE=20307617; PubMed=10848999;
 RA Sperling P., Lee M., Girke T., Zaehring U., Szyme S., Heinz E.;
 RT "A bifunctional delta 6-fatty acyl acetylenase/desaturase from the
 RT moss Ceratodon purpureus. A new member of the cytochrome b5
 RT superfamily.";
 RL Eur. J. Biochem. 267:3801-3811(2000).
 DR EMBL; AJ250735; CAB94993.1; -;
 DR InterPro: IPR001199; -;
 DR Pfam: PF00173; heme_1; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 SQ SEQUENCE 520 AA; 59160 MW; 5A9332BEC15439 CRC64;

Query Match 100.0%; Score 32; DB 10; Length 520;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDELH 5
 Db 249 HDELH 253

RESULT 8
 O9ZNMW2

ID 09ZNMW2 PRELIMINARY; PRT; 525 AA.
 AC 09ZNMW2;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE DELTA6-ACYL-LIPID DESATURASE.
 GN DES6.
 OS Physcomitrella patens (Moss).
 OC Eukaryota; Viridiplantae; Embryophyta; Bryopsida;
 OC Funariidae; Funariales; Funariaceae; Physcomitrella.
 NCBI_TaxID=3218;
 RN NCB1_TaxID=3218;
 RP SEQUENCE FROM N.A.
 RC STRAIN=HEM. B. S. G.;
 RX MEDLINE=98416756; PubMed=9744093;
 RA Girke T., Schmidt H., Zaehring U., Reski R., Heinz E.;
 RT "Identification of a novel delta 6-acyl-group desaturase by targeted
 RT gene disruption in Physcomitrella patens.";
 RL Plant J. 15:39-48(1998).
 CC -1- SIMILARITY: TO CYTOCHROME B5 DOMAIN.
 DR EMBL; AJ222981; CA11033.1; -;
 DR EMBL; AJ222980; CA11032.1; -;
 DR HSSP; P04166; 1B5M.
 DR InterPro: IPR001199; -;
 DR Pfam: PF00173; heme_1; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 525 AA; 59369 MW; 530F158B0C97C83F CRC64;

Query Match 100.0%; Score 32; DB 10; Length 525;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDELH 5
 Db 254 HDELH 258

RESULT 9
 ID P94896 PRELIMINARY; PRT; 560 AA.
 AC P94896;
 DT 01-MAY-1997 (TREMblrel. 03, Created)
 DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE ALPHA-ACETOLACTATE SYNTHASE (EC 4.1.3.18).
 GN ALS.
 OS *Oenococcus oeni* (Leuconostoc oenos).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
 OC *Oenococcus*.
 NCBI_TaxID=1247;
 RN NCB1_TaxID=1247;
 RP SEQUENCE FROM N.A.
 RC STRAIN=LO 84.13;
 RX MEDLINE=97132647; PubMed=8978099;
 RA Garwyn D., Monnet C., Martineau B., Guzzo J., Cavin J.F., Divies C.;
 RT "Cloning and sequencing of the gene encoding alpha-acetolactate
 RT decarboxylase from *Leuconostoc oenos*.";
 RL FEMS Microbiol. Lett. 145:445-450(1996).
 CC -1- CATALYTIC ACTIVITY: 2-ACETOLACTATE + CO(2) -> 2 PYRUVATE.
 CC -1- COFACTOR: THIAMIN PYRROPHOSPHATE.
 CC -1- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE THIAMINE
 CC PYRROPHOSPHATE.
 DR EMBL; X93091; CAA63640.1; -;
 DR InterPro: IPR000399; -;
 DR Pfam: PF00205; TPP_enzymes; 1.
 DR PROSITE: PS00187; TPP_ENZYMES; UNKNOWN_1.
 KW Flavoprotein; lyase; Thiamine pyrophosphate.
 SQ SEQUENCE 560 AA; 61459 MW; CADC2C1C181C0D1A CRC64;

Query Match 100.0%; Score 32; DB 2; Length 560;

Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HDPFLH 5
DB 225 HDPFLH 229

RESULT 10

004089 PRELIMINARY; PRT: 582 AA.
AC 004089.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE D9461.26P.
GN D9461.26 OR DOT1.
OS Saccharomyces cerevisiae (baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Dietrich F.S.;
RL Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E., Berno A.,
RA Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,
RA Hunkeler-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Oelner P., Oh C., Petel F.X.,
RA Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,
RA Winant A., Yelton M., Botstein D., Davis R.W.;
RL Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Jia Y., Cherry J.M.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U33007; AAB64868.1; -;
DR SGD; S0002848; DOT1.
SQ SEQUENCE 582 AA; 66201 MW; 05CA6A8F8CBAB9A CRC64;

Query Match 100.0%; Score 32; DB 3; Length 582;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDPFLH 5
DB 343 HDPFLH 347

RESULT 11

09NVN4 PRELIMINARY; PRT: 609 AA.
AC 09NVN4.
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CDNA FLJ10619 FIS, CLONE NT2RP2005472.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
RA Tanai H., Kimata M., Matanabe M., Hiraoka S., Ishii S., Kawai Y.,
RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
RA Masuko Y., Kanehori K.;
RL "NEO human cDNA sequencing project";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK001481; BAA91716.1; -;
DR InterPro; IPR000449; -;
DR Pfam; PF00627; UBA; 1;
SQ SEQUENCE 609 AA; 67866 MW; AC3C8BB09410E609 CRC64;

Query Match 100.0%; Score 32; DB 4; Length 609;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDPFLH 5
DB 149 HDPFLH 153

RESULT 12

09LUL4 PRELIMINARY; PRT: 717 AA.
AC 09LUL4.
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE SERINE/THREONINE PROTEIN KINASE-LIKE PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RX MEDLINE=20277480; PubMed=10819329;
RT Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:131-135(2000).
DR EMBL; AB022220; BAB01040.1; -;
DR InterPro; IPR000719; -;
DR InterPro; IPR001245; -;
DR InterPro; IPR001611; -;
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00560; LRR; 3.
DR PRINTS; PR00019; LEURICHRPT.
DR PROSITE; PS00109; TYRKINASE.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR SMART; SM00221; STYK; 1.
KW ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
SQ SEQUENCE 717 AA; 77634 MW; 5CECAC43C1D81E37 CRC64;

Query Match 100.0%; Score 32; DB 10; Length 717;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDPFLH 5
DB 503 HDPFLH 507

RESULT 13

054810 PRELIMINARY; PRT: 917 AA.
AC 054810.
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE ERCC4_MOUSE.
GN ERCC-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Adamson A.W.,
RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Ganes J., Dangnan L., Poundstone P.,
RA Christensen M., Georgescu A., Avila J., Liu S., Atlix C., Andreise T.,
RA Tranhelem M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,
RA Bruce R., Thomas P., Quan G., Krommiller B., Arellano A.,
RA Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,
RA Carrano A.V.;
RL Submitted (FEF-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC004155; AAC03240.1; -;
DR InterPro; IPR002106; -;
DR PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
SQ SEQUENCE 917 AA; 103689 MW; 2206DC264BC4E233 CRC64;

Query Match 100.0%; Score 32; DB 11; Length 917;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDFLH 5
Db 899 HDFLH 903

RESULT 14
O9QZD4
ID O9QZD4 PRELIMINARY; PRT; 917 AA.
AC O9QZD4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE DNA REPAIR ENDONUCLEASE XPF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Shannon M., Lamerdin J.E., McCutchen-Maloney S.L., Richardson L.,
RA Hwang M.H., Thelen M.P., Handel M.A., Stubbs L., Thelen M.P.;
RT "Characterization of the Mouse Xpf DNA Repair Gene and Differential
RT Expression During Spermatogenesis.";
RL Genomics 0:0-0(1999)
DR EMBL; AF189285; AAF03157.1; -;
DR InterPro; IPR002106; -;
DR PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
KW Endonuclease.
SQ SEQUENCE 917 AA; 103688 MW; 8FC0A6C6F2D855B CRC64;

Query Match 100.0%; Score 32; DB 11; Length 917;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDFLH 5
Db 899 HDFLH 903

RESULT 15
O9UGA1
ID O9UGA1 PRELIMINARY; PRT; 918 AA.
AC O9UGA1;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE HYPOTHETICAL 105.1 KDA PROTEIN (FRAGMENT).
GN DKFZP586G0518.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=UTERUS;
RA Wamburt R., Heubner D., Newes H.W., Gaassenhuber J., Wiemann S.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050092; CAB43264.1; -;
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 918 AA; 105106 MW; F4B1854568E4FE11 CRC64;

Query Match 100.0%; Score 32; DB 4; Length 918;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDFLH 5
Db 435 HDFLH 439

Search completed: August 9, 2001, 20:36:17
Job time: 716 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 9, 2001, 20:24:15 ; Search time 79.24 seconds
(without alignments)
7.651 Million cell updates/sec

Title: US-09-367-013b-2_COPY_204_213

Perfect score: 73
Sequence: 1 WVKDKHNTNH 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq_0601:*

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4: /SIDSR/gcgdata/geneseq/AA1983.DAT:*

5: /SIDSR/gcgdata/geneseq/AA1984.DAT:*

6: /SIDSR/gcgdata/geneseq/AA1985.DAT:*

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9: /SIDSR/gcgdata/geneseq/AA1988.DAT:*

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20: /SIDSR/gcgdata/geneseq/AA1999.DAT:*

21: /SIDSR/gcgdata/geneseq/AA2000.DAT:*

22: /SIDSR/gcgdata/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	73	100.0	355	19	Desaturase enzyme
2	73	100.0	443	20	Caenorhabditis ele
3	73	100.0	457	19	AAW84137
4	73	100.0	457	20	AAW95504
5	73	100.0	457	20	AAW85121
6	73	100.0	457	21	AAW92599
7	73	100.0	457	21	AAW56045
8	73	100.0	457	22	AAW31684
9	73	100.0	473	21	AAW51353
10	63	86.3	525	21	AAW51354
11	63	86.3	525	22	AAW46810

12	60	82.2	520	22	AAW46440
13	59	80.8	462	21	AAW71552
14	59	80.8	469	21	AAW71555
15	57	78.1	448	21	AAW71551
16	57	78.1	483	22	AAW46435
17	57	78.1	483	22	AAW46436
18	54	74.0	422	21	AAW96722
19	53	72.6	68	21	AAW83244
20	53	72.6	222	21	AAW51352
21	53	72.6	253	21	AAW71553
22	53	72.6	446	20	AAW85122
23	53	72.6	448	17	AAW98455
24	53	72.6	448	19	AAW67471
25	53	72.6	448	20	AAW98130
26	53	72.6	448	21	AAW51349
27	52	71.2	76	21	AAW83238
28	52	71.2	104	19	AAW84140
29	52	71.2	224	21	AAW51350
30	52	71.2	252	19	AAW84141
31	52	71.2	284	21	AAW51351
32	52	71.2	326	21	AAW92921
33	52	71.2	326	21	AAW53863
34	52	71.2	353	21	AAW67393
35	52	71.2	353	21	AAW53862
36	52	71.2	449	21	AAW67392
37	52	71.2	449	21	AAW92920
38	52	71.2	449	21	AAW53861
39	52	71.2	449	21	AAW51333
40	52	71.2	449	21	AAW51334
41	52	71.2	450	21	AAW71554
42	52	71.2	458	21	AAW51348
43	52	71.2	517	21	AAW67391
44	49	67.1	447	20	AAW21891
45	49	67.1	447	21	AAW96721

ALIGNMENTS

RESULT 1

AAW84139 standard; Peptide: 355 AA.

XX

AC AAW84139;

XX

DT 15-FEB-1999 (first entry)

XX

DE Desaturase enzyme peptide sequence.

XX

KW Fatty acid: desaturase; polyunsaturated fatty acid;

KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;

KW cancer; diabetes; eczema; platelet aggregation; vasodilation;

KW cholesterol level; endometriosis; premenstrual syndrome;

KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;

KW acute respiratory syndrome; hypertension; inflammatory skin disorder.

XX

OS Unidentified.

XX

PN W09846763-A1.

XX

PD 22-OCT-1998.

XX

PF 10-APR-1998; 98WO-US07126.

XX

PR 11-APR-1997; 97US-0834655.

XX

PA (ABBO) ABBOTT LAB.

PA (CALJ) CALGENE LLC.

XX

PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P;

PI Thurnmond J;

DR WPI; 1998-594582/50.

XX New isolated fatty acid desaturase enzymes - used for the production
PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical
PT compositions, nutritional compositions, cosmetics or animal feed
XX
XX
PS Example 2; Pages 101-102; 165pp; English.
XX
CC The present sequence represents a peptide derived from a desaturase
CC enzyme. The specification describes methods for desaturating a
CC fatty acid and for producing a desaturated fatty acid by expressing
CC increased levels of a desaturase. Desaturases can be used for
CC desaturating fatty acids. The enzymes can be used to produce
CC polyunsaturated fatty acids, which can be used for treating malnutrition,
CC in pharmaceutical compositions, in cosmetics or in animal feed. The
CC polyunsaturated fatty acids can be used for treating e.g. restenosis
CC after angioplasty, inflammation, rheumatoid arthritis, asthma, psoriasis,
CC cancer, diabetes or eczema or reduce blood pressure. They can also be
CC used to inhibit platelet aggregation, cause vasodilation, lower
CC cholesterol levels, inhibit proliferation of vessel wall smooth muscle
CC and fibrous tissue, reduce or prevent gastro-intestinal bleeding and
CC other side effects caused by non-steroidal anti-inflammatory drugs,
CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic
CC encephalomyelitis and chronic fatigue after viral infections, treat AIDS,
CC multiple sclerosis, acute respiratory syndrome, hypertension and
CC inflammatory skin disorders.

SQ Sequence 355 AA;

Query Match 100.0%; Score 73; DB 19; Length 355;

Best Local Similarity 100.0%; Pred. No. 0.00077;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWKDKHNTTH 10

Db 102 wwkdkhntth 111

RESULT 2

ID AAY17751 standard; Protein; 443 AA.

XX AAY17751;

DT 11-AUG-1999 (first entry)

DE Caenorhabditis elegans Delta 6 desaturase Ced6.1.

XX Caenorhabditis elegans; C. elegans; Delta 6 desaturase; Ced6.1;
KW gamma-linolenic acid; GLA; plant fatty acid; octadecatetraenoic acid;
KW OTA; eicosanoid; eczema; mastalgia; atherosclerosis; coronary disease;
KW hypercholesterolemia; diabetic neuropathy; viral infection; acne;
KW hypertension; cirrhosis; cancer.

XX Caenorhabditis elegans.

XX MO9927111-A1.

XX 03-JUN-1999.

XX 24-NOV-1998; 98WO-GB03507.

XX 24-NOV-1997; 97GB-0024783.

XX (UYBR-) UNIV BRISTOL.

XX Napier JA;

XX WPI; 1999-370905/31.

XX N-PSDB; AAX76589.

XX Desaturase enzymes, the genes encoding them and their uses

PS Claim 1; Fig 1; 44pp; English.

XX The present sequence is Caenorhabditis elegans Delta 6 desaturase,
CC designated Ced6.1. Desaturase enzymes (I) may be used as immunogens to
CC raise and select antibodies (which may be used in immunoassays, and
CC diagnostic tests to detect the presence of (I) in a sample, or to purify
CC (I)) or as a selectable marker for transformation, especially
CC transformations involving plants. (I) can be used to produce gamma-
CC linolenic acid (GLA) (and derivatives of it), which is a high value
CC plant fatty acid that is widely used in medicine for the preparation of
CC compositions for treating disorders associated with deficiencies in GLA
CC or deficiencies in metabolites derived in vivo from GLA, such as
CC octadecatetraenoic acid (OTA) and eicosanoids. Disorders that may be
CC treated with GLA and OTA include eczema, mastalgia, atherosclerosis,
CC hypercholesterolemia, coronary disease, diabetic neuropathy, viral
CC infections, acne, hypertension, cirrhosis and cancer. The nucleotide
CC sequences (II) encoding (I) may be used as probes or primers. Probes may
CC be used to identify and purify nucleic acids and so may be used in
CC diagnosis to detect the presence of (II) in a sample. Primers are useful
CC for amplifying DNA by polymerase chain reaction (PCR). (II) may also be
CC used to prepare an organism that is either chill resistant or that
CC accumulates GLA or metabolites derived from GLA. Hybridizing DNA
CC molecules may be used as anti-sense molecules to alter the expression of
CC (II) by binding to it and preventing transcription. Hybridizing
CC molecules may also be provided as ribozymes which regulate expression by
CC cleaving RNA molecules.

SQ Sequence 443 AA;

Query Match 100.0%; Score 73; DB 20; Length 443;

Best Local Similarity 100.0%; Pred. No. 0.00099;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWKDKHNTTH 10

Db 200 wwkdkhntth 209

RESULT 3

ID AAW84137 standard; Protein; 457 AA.

XX AAW84137;

DT 15-FEB-1999 (first entry)

DE A delta-6 desaturase enzyme.

XX Fatty acid; delta-6 desaturase; polyunsaturated fatty acid;
KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
KW cholesterol level; endometriosis; premenstrual syndrome;
KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
KW acute respiratory syndrome; hypertension; inflammatory skin disorder.

XX Mortierella alpina.

XX MO9846763-A1.

XX 22-OCT-1998.

XX 10-APR-1998; 98WO-US07126.

XX 11-APR-1997; 97US-0834655.

XX (ABBO) ABBOTT LAB.

XX (CALJ) CALGENE LLC.

XX Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P;

XX WPI; 1998-594582/50.

DR N-PSDB; AAV63624.
 XX
 PT New isolated fatty acid desaturase enzymes - used for the production
 PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical
 PT compositions, nutritional compositions, cosmetics or animal feed
 XX
 PS Claim 3; Fig 3A-E; 165pp; English.
 XX
 CC The present sequence represents a Mortierella alpina fatty acid delta-6
 CC desaturase enzyme. The enzyme sequence is used in the methods of
 CC the invention. The specification describes methods for desaturating a
 CC fatty acid and for producing a desaturated fatty acid by expressing
 CC increased levels of a desaturase. The present desaturase is an enzyme
 CC which introduces a double bond carbons 6 and 7 from the carboxyl end of
 CC a fatty acid molecule. The enzyme can be used for desaturating fatty
 CC acids. The enzyme can be used to produce polyunsaturated fatty acids,
 CC which can be used for treating malnutrition, in pharmaceutical
 CC compositions, in cosmetics or in animal feed. The polyunsaturated fatty
 CC acids can be used for treating e.g. restenosis after angioplasty,
 CC inflammation, rheumatoid arthritis, asthma, psoriasis, cancer, diabetes
 CC or eczema or reduce blood pressure. They can also be used to inhibit
 CC platelet aggregation, cause vasodilation, lower cholesterol levels,
 CC inhibit proliferation of vessel wall smooth muscle and fibrous tissue,
 CC reduce or prevent gastro-intestinal bleeding and other side effects
 CC caused by non-steroidal anti-inflammatory drugs, prevent or treat
 CC endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis
 CC and chronic fatigue after viral infections, treat AIDS, multiple
 CC sclerosis, acute respiratory syndrome, hypertension and inflammatory skin
 CC disorders.
 XX
 SQ Sequence 457 AA;
 XX
 Query Match 100.0%; Score 73; DB 19; Length 457;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WMRKHNTHH 10
 |||||
 DB 204 WMRKHNTHH 213
 RESULT 4
 AAW95504
 ID AAW95504 standard; peptide: 457 AA.
 XX
 AC AAW95504;
 XX
 DT 26-MAR-1999 (first entry)
 XX
 DE Mortierella alpina delta 6 desaturase.
 XX
 KW Delta 6 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil;
 KW polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;
 KW stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula;
 KW dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;
 KW rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;
 KW diabetes; cosmetic; animal feed.
 XX
 XX Mortierella alpina.
 OS
 PN MO9846764-A1.
 XX
 PD 22-OCT-1998.
 XX
 PF 10-APR-1998; 98WO-US07421.
 XX
 PR 24-OCT-1997; 97US-0956985.
 PR 11-APR-1997; 97US-0833610.
 PR 11-APR-1997; 97US-0834033.
 PR 11-APR-1997; 97US-0834655.
 XX
 PA (ABBO) ABBOTT LAB.

PA (CALJ) CALGENE LLC.
 XX
 PI Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P;
 PI Thurmond J;
 XX
 DR WPI; 1999-080739/07.
 DR N-PSDB; AAX00889.
 XX
 PT Nucleic acid construct able to express fatty acid desaturase in
 PT plants - useful in human or animal nutrition, as cosmetics and
 PT therapeutically, e.g. for restenosis, cancer and diabetes
 XX
 PS Claim 7; Fig 3A-E; 210pp; English.
 XX
 CC This represents a Mortierella alpina delta 6 desaturase. The invention
 CC relates to a nucleic acid construct that contains at least one of the
 CC nucleotide sequences (AAX00889 to AAX00891) encoding M. alpina delta 6,
 CC delta 12 and delta 5 desaturases (AAW95504 to AAW95506) respectively,
 CC coupled to an expression control sequence functional in plants.
 CC Recombinant plant cells containing at least one DNA encoding a M. alpina
 CC fatty acid desaturase (FAD), can be used for the production of
 CC polyunsaturated fatty acid (PUFA). These recombinant cells or plants
 CC containing them are used to produce oils such as linoleic acid,
 CC arachidonic acid, gamma-linolenic acid, dihomogamma-linolenic acid,
 CC stearidonic acid and eicosapentaenoic acid (EPA). These plant oils are
 CC used: (i) to treat malnutrition; (ii) in infant feeding formulas, or
 CC dietary supplements or substitutes, for use in humans or animals; (iii)
 CC for treating disorders associated with inadequate consumption or
 CC production of PUFA (or their metabolites such as prostaglandins), e.g.
 CC restenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis,
 CC psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics, and
 CC (v) as animal feeds. Fragments of the DNA are used as probes to isolate
 CC related coding sequences. Recombinant plants can produce high yields of
 CC PUFA, since new pathways can be created and unwanted ones suppressed.
 CC Plants can be engineered to express oils of particular PUFA composition,
 CC e.g. one similar to that in human milk, and product recovery is simpler
 CC than with e.g. fish.
 XX
 SQ Sequence 457 AA;
 XX
 Query Match 100.0%; Score 73; DB 20; Length 457;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WMRKHNTHH 10
 |||||
 DB 204 WMRKHNTHH 213
 RESULT 5
 AAW85121
 ID AAW85121 standard; Protein; 457 AA.
 XX
 AC AAW85121;
 XX
 DT 11-FEB-1999 (first entry)
 XX
 DE A delta-6 desaturase enzyme amino acid sequence.
 XX
 DE Fatty acid: delta-6 desaturase; polyunsaturated fatty acid;
 KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
 KW cholesterol level; endometriosis; premenstrual syndrome;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
 XX
 OS Unidentified.
 XX
 PN MO9846765-A1.
 XX
 PD 22-OCT-1998.
 XX

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PF 10-APR-1998; 98WO-US07422.
XX
XX 11-APR-1997; 97US-0833610.
XX
XX (ABBO ) ABBOTT LAB.
PA (CALJ ) CALGENE LLC.
XX
XX Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P;
PI Thurmond J;
XX
XX WPI; 1999-009334/01.
XX
XX New nucleic acid encoding delta5 and other desaturase enzymes -
PT useful in production of oils of increased arachidonic acid content,
PT used, e.g. for treating cancer, as foods, animal feeds and cosmetics
XX
XX Disclosure: Pages 95-96; 153pp; English.
XX
XX The present sequence represents a fatty acid delta-6 desaturase enzyme.
CC The specification describes methods for desaturating a fatty acid and
CC for producing a desaturated fatty acid by expressing increased levels of
CC a desaturase. The present desaturase is an enzyme which introduces a
CC double bond carbons 6 and 7 from the carboxyl end of a fatty acid
CC molecule. The enzyme can be used for desaturating fatty acids. The
CC enzyme can be used to produce polyunsaturated fatty acids, which can
CC be used for treating malnutrition. In pharmaceutical compositions,
CC in cosmetics or in animal feed. The polyunsaturated fatty acids can
CC be used for treating e.g. restenosis after angioplasty, inflammation,
CC rheumatoid arthritis, asthma, psoriasis, cancer, diabetes or eczema
CC or reduce blood pressure. They can also be used to inhibit platelet
CC aggregation, cause vasodilation, lower cholesterol levels, inhibit
CC proliferation of vessel wall smooth muscle and fibrous tissue,
CC reduce or prevent gastro-intestinal bleeding and other side effects
CC caused by non-steroidal anti-inflammatory drugs, prevent or treat
CC endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis
CC and chronic fatigue after viral infections, treat AIDS, multiple
CC sclerosis, acute respiratory syndrome, hypertension and inflammatory skin
CC disorders.
XX
XX Sequence 457 AA:
SQ

```

Query Match 100.0%; Score 73; DB 20; Length 457;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WKKDKHNTHH 10
|||||
Db 204 wkkdkhntnh 213

RESULT 6
AA92599
ID AA92599 standard; Protein: 457 AA.
XX
XX AA92599;
XX
XX 10-AUG-2000 (first entry)
XX
XX M. alpina delta-6 fatty acid desaturase.
XX
XX delta-6 desaturase; gamma-linolenic acid; biosynthesis;
KW transgenic insect cell; polyunsaturated long chain fatty acid;
KW antiinflammatory; antihemetic; antispasmodic; antipruritic;
KW osteopathic; cytosolic; antidiabetic; dermatological; gynecological;
KW anti-HIV; neuroprotective; hypotensive; nephrotoxic; vasodilator;
KW antiagregant; vasotropic.
XX
XX Mortierella alpina.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 172..176
XX FT /Label= histidine_box

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FT /note="conserved among membrane-bound desaturases"
FT FT Misc-difference 209...213
FT FT /Label= histidine_box
FT FT /note="conserved among membrane-bound desaturases"
FT FT Misc-difference 395..399
FT FT /Label= histidine_box
FT FT /note="conserved among membrane-bound desaturases"
XX
XX W0200020602-A2.
XX
XX 13-APR-2000.
XX
XX 29-SEP-1999; 99WO-US22686.
XX
XX 05-OCT-1998; 98US-0103110.
XX
XX (ABBO ) ABBOTT LAB.
XX
XX Mukerji P, Huang Y, Parker-barnes JM, Das T;
PI
XX
XX WPI; 2000-328935/28.
XX
XX N-PSDB; AAA09430.
XX
XX Novel transgenic insect cells comprising a nucleotide sequences which
PT encode delta-6-desaturase or delta-12- desaturase, useful for producing
PT poly-unsaturated long chain fatty acids, e.g. arachidonic acid
XX
XX Claim 1; Page 145-146; 170pp; English.
XX
XX The fatty acid desaturases are able to catalyse the conversion of oleic
XX acid to linoleic acid, linoleic acid to gamma-linolenic acid or of
XX alpha-linolenic acid to stearidonic acid. Transgenic insect cells
XX comprising a nucleotide sequence which encodes a polypeptide comprising
XX .residues 50-53, 39-43, 172-176, 204-213, or 390-402 of delta-6
XX desaturase (AA92599) or comprising delta-12 desaturase (AA92600) are
XX claimed. Oil and fatty acids (especially gamma-linolenic acid) isolated
XX from the recombinant insect cells are also claimed. Production of
XX polyunsaturated long chain fatty acids (PUFAs) in insect cells has many
XX advantages, as insect cells have greatly simplified lipid compositions,
XX are not subject to external variable fluctuations, and can easily be
XX maintained and manipulated. The oils are used in pharmaceutical
XX compositions, infant formulas, dietary supplements or substitutes, and
XX cosmetics (all claimed). The PUFA supplements have antiinflammatory,
XX antirheumatic, antispasmodic, antipruritic, osteopathic, cytosolic,
XX antidiabetic, dermatological, gynecological, anti-HIV, neuroprotective,
XX hypotensive, nephrotoxic, vasodilator, antiagregant and vasotropic
XX activity.
XX
XX Sequence 457 AA:
SQ

```

Query Match 100.0%; Score 73; DB 21; Length 457;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WKKDKHNTHH 10
|||||
Db 204 wkkdkhntnh 213

RESULT 7
AA56045
ID AA56045 standard; Protein: 457 AA.
XX
XX AA56045;
XX
XX 28-MAR-2000 (first entry)
XX
XX Fungal delta6-desaturase protein sequence.
XX
XX Polyunsaturated fatty acid; fungus; delta6-desaturase; animal feed;
KW transgenic animal; malnutrition; biosynthesis.
XX

OS Unidentified.
 XX
 PN WO961602-A1.
 XX
 PD 02-DEC-1999.
 XX
 PF 28-MAY-1999; 99MO-US12088.
 XX
 PR 29-MAY-1998; 98US-0087578.
 XX
 PA (OHIS) UNIV OHIO STATE.
 XX
 PI Kopchick JJ, Kelder B, Huang Y, Kirchner SJ, Mukerji P;
 XX
 DR WPI; 2000-072619/06.
 DR N-PSDB; AA247129.
 XX
 PT Producing essential fatty acids and long-chain polyunsaturated fatty
 PT acids, for use in nutritional, animal feed and medical formulations -
 XX
 PS Disclosure; Fig 9; 71pp; English.
 XX
 CC The invention relates to a method of generating novel compositions
 CC comprising animal cells producing essential fatty acids (FAs). The animal
 CC cells are produced by transforming cells, e.g. embryonic stem cells, with
 CC nucleic acid encoding heterologous enzymes involved in fatty acid,
 CC e.g. long chain or polyunsaturated fatty acid (PPA) biosynthesis. This
 CC sequence corresponds to a fungal delta6-desaturase whose coding sequence
 CC is an example of a nucleic acid sequence used to transform the cells. The
 CC essential FAs obtained can be used in nutritional formulations or animal
 CC feed formulations. The long chain PFAs can be used in nutritional
 CC formulations, cosmetic formulations or animal feed formulations. The
 CC products can also be used for producing transgenic animals which can be
 CC used for producing essential FAs which can be used for producing
 CC downstream products such as leukotrienes, thromboxanes, arachidonic acid,
 CC eicosapentaenoic acid or docosahexaenoic acid. The products can also be
 CC used in cell culture. The animal or milk fat produced can be administered
 CC to treat malnutrition.
 CC
 SQ Sequence 457 AA:
 Query Match 100.0%; Score 73; DB 21; Length 457;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WVKDKHNTTH 10
 DB 204 WVKDKHNTTH 213
 RESULT 8
 AAB31684
 ID AAB31684 standard; Protein; 457 AA.
 XX
 AC AAB31684;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE Amino acid sequence of a fungal delta6 desaturase.
 XX
 KM delta6 desaturase; desaturase gene; elongase gene; fatty acid;
 KM eicosanoid; nutrition; infant formula; dietary supplement;
 KM dietary substitute; animal feed.
 XX
 OS Mortierella alpina.
 XX
 PN WO200104636-A1.
 XX
 PD 18-JAN-2001.
 XX
 PF 11-JUL-2000; 2000MO-US19011.
 XX

PR 12-JUL-1999; 99US-0351525.
 XX
 PA (UYOH-) UNIV OHIO.
 XX
 PI Kopchick JJ, Kelder B;
 XX
 DR WPI; 2001-182622/18.
 DR N-PSDB; AAF25234.
 XX
 PT New compositions comprising cells that express desaturases and
 PT elongases, for synthesizing essential fatty acids or long-chain
 PT polyunsaturated fatty acids, used in nutritional, cosmetic or animal
 PT feed formulations -
 XX
 PS Disclosure; Fig 9; 93pp; English.
 XX
 CC The present sequence represents a delta6 desaturase. The desaturase
 CC polynucleotide sequence was used to transfect mammalian cells, to
 CC produce animal cells expressing a desaturase gene and/or an elongase
 CC gene. Compositions comprising cells of the invention are useful for
 CC synthesizing essential fatty acids, their derivatives or downstream
 CC products, as well as altered levels of long-chain polyunsaturated
 CC fatty acids and eicosanoids. The compositions are useful in nutritional
 CC formulae, e.g. infant formula, dietary supplements or dietary
 CC substitutes for both humans and animals. The compositions are also
 CC useful in cosmetic or animal feed formulations. Furthermore, the
 CC compositions may also be used as fat free media or as research reagents.
 XX
 SQ Sequence 457 AA:
 Query Match 100.0%; Score 73; DB 22; Length 457;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WVKDKHNTTH 10
 DB 204 WVKDKHNTTH 213
 RESULT 9
 AAY51353
 ID AAY51353 standard; Protein; 473 AA.
 XX
 AC AAY51353;
 XX
 DT 27-APR-2000 (first entry)
 XX
 DE Protein b5case with delta6 fatty acid desaturase activity.
 XX
 KM Sphingolipid desaturase; sld; sphingobase; ceramide; capnoid;
 KM transgenic plant; crop plant; delta-8-unsaturated long-chain base;
 KM tolerance; resistance; soil salinity; ion stress; toxicity; drought;
 KM cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
 KM pharmaceutical; food; chemical raw material.
 XX
 OS Unidentified.
 XX
 PN DE19828850-A1.
 XX
 PD 30-DEC-1999.
 XX
 PF 27-JUN-1998; 98DE-1028850.
 XX
 PR 27-JUN-1998; 98DE-1028850.
 XX
 (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
 XX
 PI Heinz E, Zehringer U, Schmidt H, Sperling P;
 XX
 DR WPI; 2000-127549/12.
 XX
 PT New sphingolipid desaturase that selectively introduces double bond

PT Into sphingolipids and capnoids -
XX
PS Disclosure: Page 38-39; 62pp; German.
XX
CC This invention describes a novel sphingolipid desaturase that selectively
CC introduces a double bond into the sphingobase of the ceramide residue of
CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
CC desaturase, or a vector containing the DNA sequence, can be used to
CC produce transgenic plants, especially crop plants, with an increased or
CC decreased delta-8-unsaturated long-chain base content or an altered
CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
CC compensate for a delta-8-unsaturated long-chain base deficiency, to
CC exclude production of delta-8-unsaturated bases, to increase tolerance
CC or resistance to soil salinity, ion stress or toxicity, drought, wet
CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
CC alter size growth and flowering time. Cells, transgenic organisms or
CC plants containing the DNA sequence can be used to produce sphingolipids
CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
CC materials. This sequence represents a protein which has delta6 fatty acid
CC desaturase activity which is described in the method of the invention.
XX
SQ Sequence 473 AA:

Query Match 100.0%; Score 73; DB 21; Length 473;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WNKDKHNTHH 10
ID AAB46810 standard; Protein; 525 AA.
DB 230 wwkdkhnthh 239

RESULT 10

ID AAY51354 standard; Protein; 525 AA.

AC AAY51354;

DT 27-APR-2000 (first entry)

DE Protein b5pp with delta6 fatty acid desaturase activity.

XX Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid;

KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;

KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;

KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;

KW pharmaceutical; food; chemical raw material.

OS Unidentified.

XX DE19828850-A1.

PD 30-DEC-1999.

PF 27-JUN-1998; 98DE-1028850.

PR 27-JUN-1998; 98DE-1028850.

PA (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.

PI Heinz E, Zaehrer U, Schmidt H, Sperling P;

PS Disclosure: Fig 16; 62pp; German.

CC This invention describes a novel sphingolipid desaturase that selectively
CC introduces a double bond into the sphingobase of the ceramide residue of

CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
CC desaturase, or a vector containing the DNA sequence, can be used to
CC produce transgenic plants, especially crop plants, with an increased or
CC decreased delta-8-unsaturated long-chain base content or an altered
CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
CC compensate for a delta-8-unsaturated long-chain base deficiency, to
CC exclude production of delta-8-unsaturated bases, to increase tolerance
CC or resistance to soil salinity, ion stress or toxicity, drought, wet
CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
CC alter size growth and flowering time. Cells, transgenic organisms or
CC plants containing the DNA sequence can be used to produce sphingolipids
CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
CC materials. This sequence represents a protein which has delta6 fatty acid
CC desaturase activity which is described in the method of the invention.
XX
SQ Sequence 525 AA:

Query Match 86.3%; Score 63; DB 21; Length 525;
Best Local Similarity 80.0%; Pred. No. 0.041;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WNKDKHNTHH 10
ID AAB46810 standard; Protein; 525 AA.
DB 286 wwkdkhnthh 295

RESULT 11

ID AAB46810 standard; Protein; 525 AA.

AC AAB46810;

DT 23-APR-2001 (first entry)

DE P. patens delta6-desaturase protein.

XX Delta6-desaturase; unsaturated fatty acid; transgenic; oil; lipid;

KW fatty acid; human nutrition; animal nutrition; cosmetic; pharmaceutical;

KW agricultural chemical.

XX Physcomitrella patens.

OS WO200102591-A1.

PD 11-JAN-2001.

PF 04-JUL-2000; 2000WO-EP06223.

PR 06-JUL-1999; 99US-0347531.

PA (BADI) BASF AG.

PI Heinz E, Girke T, Scheffler J, Da Costa Silva EO;

PS WPI: 2001-123117/13.

PT Production of unsaturated fatty acids, useful e.g. in nutrition,

PT cosmetics or pharmaceuticals, in organisms transformed with

PT Physcomitrella patens delta-6-desaturase nucleic acid -

PS Claim 1c; Page 41-43; 49pp; German.

CC This invention describes a novel preparation of unsaturated fatty acids
CC (II) by introducing into an organism at least one isolated nucleic acid
CC (II) that encodes a polypeptide (III) with Delta6-desaturase activity.
CC Organisms that contain at least 1 wt. % (I), on total fatty acid content,
CC are then selected. (II) is selected from: (a) a 2012 bp sequence (S1),
CC defined in the specification, or its equivalents within the degeneracy of
CC the genetic code; or (b) derivatives of the sequence of (a) that encode a

CC 525 amino acid polypeptide (S2), defined in the specification, or a
 CC polypeptide with at least 50% homology with (S2) and practically the same
 CC enzymatic activity. The invention also describes (1) transgenic organisms
 CC that contain (II); and (2) oils, lipids and fatty acids produced by the
 CC new method. The oils, lipids and fatty acids produced by the transformed
 CC organisms are used in human or animal nutrition, cosmetics,
 CC pharmaceuticals and agricultural chemicals. (III) can also be used, in
 CC vitro, for increasing the (I) content of triglycerides. The transgenic
 CC organisms have increased contents of (I), or of (I)-containing
 CC triglycerides, particularly of gamma-linolenic acid.

XX Sequence 525 AA;

Query Match 86.3%; Score 63; DB 22; Length 525;
 Best Local Similarity 80.0%; Pred. No. 0.041;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WMKDKHNTTH 10
 ||| ||| ||
 Db 286 wvkeknhlh 295

RESULT 12

AAB46440
 ID AAB46440 standard; Protein; 520 AA.

XX AAB46440;

DT 06-APR-2001 (first entry)

XX C. purpureus delta6-acetylenase/delta6-desaturase SEQ ID NO 12.

DE Delta6-acetylenase: delta6-desaturase; unsaturated fatty acid;

XX transgenic plant; plant oil; triglyceride; nutrition; animal feed;

KW cosmetic.

XX Ceratodon purpureus.

OS WO200075341-A1.

XX 14-DEC-2000.

PD 07-JUN-2000; 2000WO-EP05274.

XX 07-JUN-1999; 99DE-1025718.

PR 22-DEC-1999; 99DE-1062409.

XX (BADI) BASF AG.

PA Heinz E, Szyme S, Lee M, Garke T, Sperling P, Zaehring U;

PI WPI; 2001-112150/12.

DR N-PSDB; AAF25734.

XX Nucleic acid encoding delta6-acetylenase or desaturase, useful for

PT producing plant oils with increased content of unsaturated fatty acids

PT -

XX Example 7; Page 57-59; 69pp; German.

PS This invention describes a novel isolated nucleic acid (I) encoding

XX polypeptide (II) with Delta6-acetylenase and/or Delta6-desaturase

CC activity. The invention also describes (a) amino acid sequences encoded

CC by (I); (b) an expression cassette (EC) containing (I) linked to one or

CC more regulatory sequences; (c) a vector containing (I) and EC; (d)

CC organisms containing (I), EC or the vectors of (c); (e) preparation of

CC unsaturated fatty acids (A) or triglycerides (TG) with increased content

CC of (A) by introducing (I) or EC into an oil-producing organism; (f)

CC proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)

CC production of (A) or TG by using (Ia); and (h) (A) and TG produced by

CC method (g). (I) are used to produce transgenic plants (or other

CC organisms) that produce oils or triglycerides (TG) with increased content

CC of unsaturated fatty acids (A) and to isolate related sequences by
 CC homology screening. (A), or TG containing them, are useful in human
 CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
 CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes,
 CC can be used to suppress expression of (II), resulting in oils with
 CC increased content of saturated fatty acids.

XX Sequence 520 AA;

Query Match 82.2%; Score 60; DB 22; Length 520;
 Best Local Similarity 80.0%; Pred. No. 0.12;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 WMKDKHNTTH 10
 ||| ||| ||
 Db 281 wvkeknhlh 290

RESULT 13

AAV71552
 ID AAV71552 standard; Protein; 462 AA.

XX AAV71552;

DT 12-OCT-2000 (first entry)

XX Corn sphingolipid desaturase.

XX Corn; sphingolipid desaturase; membrane-bound desaturase;

KW transgenic plant; fatty acid.

OS Zea mays.

XX WO200032790-A2.

PD 08-JUN-2000.

XX 02-DEC-1999; 99WO-US28589.

PR 03-DEC-1998; 98US-0110784.

XX (DUPO) DU PONT DE NEMOURS & CO E. I.

PI Cahoon EB, Cahoon RE, Hiltz WD, Kinney AJ;

DR WPI; 2000-412336/35.

DR N-PSDB; AAD01350.

XX Polynucleotide encoding delta-6 desaturase enzyme useful for producing

PT transgenic plants and for producing antibodies specific to which is

PT useful for screening cDNA expression libraries -

XX Claim 10; Page 42-43; 57pp; English.

XX The present sequence is a sphingolipid desaturase

CC from clone cdelc.pK001.08.fis isolated from corn developing

CC embryo cDNA library, cdelc. The present sequence is useful for producing

CC transgenic plants having altered levels of sphingolipid desaturase which

CC in turn would alter the fatty acid composition. The enzyme is also useful

CC for producing polyclonal or monoclonal antibodies. The polynucleotide

CC is useful as primer or probe for screening cDNA libraries to

CC isolate desired full-length cDNA clones.

XX Sequence 462 AA;

Query Match 80.8%; Score 59; DB 21; Length 462;
 Best Local Similarity 80.0%; Pred. No. 0.15;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 WMKDKHNTTH 10
 ||| ||| |||

DB 204 wwkcnhntnh 213

RESULT 14

ID AAY71555 standard; Protein; 469 AA.

XX AAY71555;

DT 12-OCT-2000 (first entry)

DE Wheat sphingolipid desaturase #1.

KW Wheat; sphingolipid desaturase; membrane-bound desaturase;
transgenic plant; fatty acid.

XX Triticum aestivum.

PN WO200032790-A2.

PD 08-JUN-2000.

PF 02-DEC-1999; 99WO-US28589.

PR 03-DEC-1998; 98US-0110784.

PA (DUPO) DU PONT DE NEMOURS & CO E I.

PI Cahoon EB, Cahoon RE, Hiltz WD, Kinney AJ;

DR WPI: 2000-412336/35.

DR N-PSDB; AAD01353.

PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
transgenic plants and for producing antibodies specific to which is
useful for screening cDNA expression libraries

XX Example 4; Page 49-50; 57pp; English.

CC The present sequence is a sphingolipid desaturase
from clone wrel.pk0004.c7:fls isolated from wheat etiolated
seedling root cDNA library, wrel.

CC The present sequence is useful for producing

CC transgenic plants having altered levels of sphingolipid desaturase which

CC in turn would alter the fatty acid composition. The enzyme is also useful

CC for producing polyclonal or monoclonal antibodies. The polynucleotide

CC is useful as primer or probe for screening cDNA libraries to

CC isolate desired full-length cDNA clones.

CC Sequence 469 AA;

CC

OY 1 WKKDKHNTTH 10
||| |||||
DB 211 wwkfnhntnh 220

RESULT 15

ID AAY71551 standard; Protein; 448 AA.

XX AAY71551;

DT 12-OCT-2000 (first entry)

DE Florida bitterbush delta-6 fatty acid desaturase.

KW Florida bitterbush; delta-6 fatty acid desaturase; tannic acid;
transgenic plant; fatty acid; membrane-bound desaturase.

XX Picramnia pentandra.

PN WO200032790-A2.

PD 08-JUN-2000.

PF 02-DEC-1999; 99WO-US28589.

PR 03-DEC-1998; 98US-0110784.

PA (DUPO) DU PONT DE NEMOURS & CO E I.

PI Cahoon EB, Cahoon RE, Hiltz WD, Kinney AJ;

DR WPI: 2000-412336/35.

DR N-PSDB; AAD01349.

PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
transgenic plants and for producing antibodies specific to which is
useful for screening cDNA expression libraries

PS Claim 10; Page 40-41; 57pp; English.

CC The present sequence is a delta-6 fatty acid desaturase protein sequence
from clone pps.pk0011.d5:fls isolated from Florida bitterbush developing
seed cDNA library, pps. The delta-6 desaturase enzyme catalyses the

CC formation of tannic acid, a fatty acid that has a triple bond at the

CC delta-6 carbon. The present sequence is useful for producing

CC transgenic plants having altered levels of delta-6 desaturase which

CC in turn would alter the fatty acid composition. The enzyme is also useful

CC for producing polyclonal or monoclonal antibodies. The polynucleotide

CC is useful as primer or probe for screening cDNA libraries to

CC isolate desired full-length cDNA clones.

CC Sequence 448 AA;

CC

OY 1 WKKDKHNTTH 10
||| |||||
DB 190 wwkldhntnh 199

Search completed: August 9, 2001, 20:24:16
Job time: 250 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 9, 2001, 20:26:06 ; Search time 50.69 seconds
(without alignments)
15.028 Million cell updates/sec

Title: US-09-367-013b-2_COPY_204_213

Perfect score: 73

Sequence: 1 WMKDKHNTTH 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR68:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	73	100.0	473	1 T26280	linoleoyl-CoA desat
2	523	86.3	523	3 JC7556	linoleoyl-CoA desat
3	57	78.1	345	2 T3617	probable Delta6 fa
4	52	71.2	449	2 A84900	hypothetical prote
5	52	71.2	449	2 T47950	delta-8 sphingolip
6	52	71.2	449	2 T50555	delta-8 sphingolip
7	52	71.2	458	2 S68358	Delta8 sphingolip
8	49	67.1	447	1 T43319	Delta5 fatty acid
9	44	60.3	1111	2 T01078	hypothetical prote
10	43	58.9	255	2 A33417	folate-binding pro
11	43	58.9	350	2 S43772	phosphatidylcholin
12	43	58.9	359	2 T42087	probable 6-phospho
13	43	58.9	424	2 JCS891	omega 6 desaturase
14	43	58.9	444	2 T13155	linoleoyl-CoA desat
15	43	58.9	444	2 JG0180	Delta6 fatty acid
16	43	58.9	479	2 T40925	stearyl-CoA desat
17	43	58.9	942	2 T39624	6-phosphofructokin
18	43	58.9	2671	2 A49873	inositol 1,4,5-tri
19	43	57.5	305	2 H86245	bifunctional nucle
20	42	57.5	486	2 T18228	stearyl-CoA desat
21	42	57.5	493	1 S71634	stearyl-CoA desat
22	42	57.5	510	1 S64059	stearyl-CoA desat
23	42	57.5	550	2 F86127	hypothetical prote
24	41	56.2	129	2 T47958	hypothetical prote
25	41	56.2	452	1 H65036	CDPdiacylglycerol
26	41	56.2	452	2 H85905	hypothetical prote
27	41	56.2	476	2 S52746	stearyl-CoA desat
28	41	56.2	575	2 T34280	hypothetical prote
29	41	56.2	638	2 T51383	receptor protein k

30	41	56.2	790	2 T12203	transcription fact
31	40	54.8	135	2 C70890	hypothetical prote
32	40	54.8	251	2 S67191	hypothetical prote
33	40	54.8	401	2 S37815	aureobasidin A res
34	40	54.8	410	2 C84176	oxalate/formate an
35	40	54.8	704	2 T14614	hypothetical prote
36	40	54.8	837	2 D84428	hypothetical prote
37	40	54.8	975	2 A86258	protein F5011.4 l1
38	40	54.8	1188	2 D86311	protein F113.20 l1
39	40	54.8	2670	2 A46719	inositol 1,4,5-tri
40	39.5	54.1	307	2 A35125	phospholipase D (E
41	39.5	54.1	307	2 T40839	phospholipase D (E
42	39.5	54.1	344	1 Q3ECTH	hypothetical 40.5k
43	39	53.4	126	2 H72860	probable capsid pr
44	39	53.4	126	2 T41827	p15 orf87 - Bombyx
45	39	53.4	256	2 S13338	hypothetical prote

ALIGNMENTS

RESULT 1
T26280
linoleoyl-CoA desaturase (EC 1.14.99.25) W08D2.4 - Caenorhabditis elegans
N/Alternate names: Delta6 fatty acid desaturase
C/Species: Caenorhabditis elegans
C/Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
R/Accession: T26280; T37238
R/Swinburne, J.; Almscough, R.
Submitted to the EMBL Data Library, March 1996
A/Reference number: T26280
A/Accession: T26280
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-473 <MTL>
A/Cross-references: EMBL:Z70271; PIDN:CAA94233.1; GSPDB:GN00022; CESP:W08D2.4
A/Experimental source: Clone W08D2
R/Majier, J.A.; Hey, S.J.; Lacey, D.J.; Shevry, P.R.
Biochem. J. 330, 611-614, 1998
A/Title: Identification of a caenorhabditis elegans Delta6 fatty acid desaturase by h
A/Reference number: Z21637; M0UD:98149727
A/Accession: T37238
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-38, 69-430, 'V', 432-473 <NAP>
A/Cross-references: EMBL:AF031477; NID:93088519; PIDN:AAC15586.1; PID:93088520
C/Genetics:
A/Gene: CESP:W08D2.4
A/Map position: 4
C/Insertions: 13/3; 39/2; 234/3; 277/3; 378/1; 413/3
C/Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
C/Keywords: alternative splicing; oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 100.0%; Score 73; DB 1; Length 473;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMKDKHNTTH 10
DB 230 WMKDKHNTTH 239

RESULT 2
JC7556
linoleoyl-CoA desaturase (EC 1.14.99.25) - Mucor rouxii
N/Alternate names: delta6-desaturase
C/Species: Mucor rouxii
C/Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 31-Mar-2001
R/Accession: JC7556
R/Laoteng, K.; Mannontarat, R.; Tanticharoen, M.; Cheevadhanarak, S.
Biochem. Biophys. Res. Commun. 279, 17-22, 2000
A/Title: Delta6-desaturase of Mucor rouxii with high similarity to plant delta6-desat

A:Reference number: JC7556; MUID: 20563795
A:Accession: JC7556
A:Molecule type: DNA
A:Residues: 1-523 <LAO>
A:Cross-references: GB:AF290983
A:Experimental source: strain ATCC 24905
C:Comment: This enzyme, a membrane-bound key enzyme, is responsible for the transform
C:Keywords: transformation; oxidoreductase

Query Match 86.3%; Score 63; DB 3; Length 523;
Best Local Similarity 80.0%; Pred. No. 0.013;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 WVKDKHNTHH 10
||| ||| ||
DB 265 WVKDKNHNVH 274

RESULT 3
T36617
probable Delta6 fatty acid desaturase (EC 1.14.99.-) SCH35.42c [similarity] - Streptomy
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
C:Accession: T36617
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A:Reference number: Z21610
A:Accession: T36617
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-345 <OLI>
A:Cross-references: EMBL:AL078610; PIDN:CAB44385.1; GSPDB:GN00070; SCOEDB:SCH35.42C
C:Genetics:
A:Gene: SCOEDB:SCH35.42C
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 78.1%; Score 57; DB 2; Length 345;
Best Local Similarity 70.0%; Pred. No. 0.074;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WVKDKHNTHH 10
||| ||| ||
DB 114 WVKDKHNTHH 123

RESULT 4
A84900
hypothetical protein At2g46210 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: A84900
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
Euss, D.; Nerman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: A84900
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-449 <STO>
A:Cross-references: GB:AE002093; NID:g3702328; PIDN:AAC62885.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g46210
A:Map position: 2

Query Match 71.2%; Score 52; DB 2; Length 449;
Best Local Similarity 70.0%; Pred. No. 0.61;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 WVKDKHNTHH 10
||| ||| ||
DB 192 WVKWTHNAHH 201

RESULT 5
T47950
delta-8 sphingolipid desaturase (EC 1.14.99.-) [validated] - Arabidopsis thaliana
N:Alternate names: protein F2A19.180
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C:Accession: T47950; T51848
R:De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Q
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z24480
A:Accession: T47950
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-449 <DEH>
A:Cross-references: EMBL:AL132962; PIDN:CAB71088.1
A:Experimental source: cultivar Columbia; BAC clone F2A19
R:Spierling, P.; Zaehring, U.; Heinz, E.
J. Biol. Chem. 273, 28590-28596, 1998
A:Title: A sphingolipid desaturase from higher plants. Identification of a new cytoch
A:Reference number: Z22986; MUID:99003197
A:Accession: T51848
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-449 <SPE>
A:Cross-references: EMBL:AJ224161; PIDN:CA11858.1
A:Experimental source: cultivar Columbia; mainly green parts, some flowers, few roots
C:Genetics:
A:Gene: slt1
A:Map position: 3
A>Note: F2A19.180
C:Function:
A:Description: (EC 1.14.99.-): delta-8 sphingolipid desaturase [validated; MUID:99003
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 71.2%; Score 52; DB 2; Length 449;
Best Local Similarity 70.0%; Pred. No. 0.61;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 WVKDKHNTHH 10
||| ||| ||
DB 192 WVKWTHNAHH 201

RESULT 6
T50555
delta-8 sphingolipid desaturase [imported] - rape
C:Species: Brassica napus (rape)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 15-Sep-2000
C:Accession: T50555
R:Spierling, P.; Zaehring, U.; Heinz, E.
J. Biol. Chem. 273, 28590-28596, 1998
A:Title: A sphingolipid desaturase from higher plants. Identification of a new cytoch
A:Reference number: Z22986; MUID:99003197
A:Accession: T50555
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-449 <SPE>
A:Cross-references: EMBL:AJ224160; PIDN:CA11857.1
A:Experimental source: cultivar Drakkar
C:Genetics:
A:Gene: slt1

Query Match 71.2%; Score 52; DB 2; Length 449;
Best Local Similarity 70.0%; Pred. No. 0.61;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WMKDHNTHH 10
||| ||| ||
Db 192 WMKTHNAHH 201

RESULT 7
S68358
Delta8 sphingolipid desaturase (EC 1.14.99.-) [similarity] - common sunflower
C:Species: Helianthus annuus (common sunflower)
C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
C:Accession: S68358
R:Spelling, P.; Schmidt, H.; Heinz, E.
Eur. J. Biochem. 232, 798-805, 1995
A:Title: A cytochrome-b(5)-containing fusion protein similar to plant acyl lipid desaturase
A:Reference number: S68358; MUID:96028121
A:Accession: S68358
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-458 <SPE>
A:Cross-references: EMBL:X87143; NID:q1040728; PIDN:CAA60621.1; PID:q1040729
C:Superfamily: cytochrome b5 core homology
C:Keywords: heme; iron; metalloprotein; oxidoreductase
F:16-90/Domain: cytochrome b5 core homology <CB5>
F:51,74/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 71.2%; Score 52; DB 2; Length 458;
Best Local Similarity 70.0%; Pred. No. 0.63;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WMKDHNTHH 10
||| ||| ||
Db 201 WMKTHNAHH 210

RESULT 8
T43319
Delta5 fatty acid desaturase (EC 1.14.99.-) T13F2.1 [validated] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
C:Accession: T43319; T24875
R:Michelson, L.V.; Napier, J.A.; Lewis, M.; Griffiths, G.; Lazarus, C.M.; Stobart, A.K.;
FEBS Lett. 433, 215-218, 1998
A:Title: Functional identification of a fatty acid delta5 desaturase gene from Caenorhabditis elegans
A:Reference number: Z22422; MUID:99059456
A:Accession: T43319
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-447 <MIC>
A:Cross-references: EMBL:AF078796; NID:g4003522; PIDN:AC95143.1; PID:g4003523
R:Swiburne, J.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19947
A:Accession: T24875
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-197; 'VSHIFNN', 198-447 <MIU>
A:Cross-references: EMBL:Z81122; PIDN:CA603352.1; GSPDB:GN00022; CESP:T13F2.1
A:Experimental source: clone T13F2
C:Genetics:
A:Gene: CESP:T13F2.1; des-5
A:Map position: 4
A:Insertions: 43/3; 80/3; 197/3; 295/3; 318/2; 349/1; 384/3
C:Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 67.1%; Score 49; DB 1; Length 447;
Best Local Similarity 66.7%; Pred. No. 1.8;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 WMKDHNTHH 10

Db 204 WKEQHNHH 212
||: ||| ||

RESULT 9
T01078
hypothetical protein T10P11.2.2 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 24-Mar-1999
C:Accession: T01078
R:Kaplan, N.; Johnson, D.; Schutz, K.; Gnoj, L.; Hoffman, J.; Tili, S.; de la Bastide
hl, M.; Martienssen, R.; Chen, E.Y.; Wilson, R.; McComble, W.R.
submitted to the EMBL Data Library, November 1998
A:Description: Sequence of A. thaliana BAC T10P11 from chromosome IV.
A:Reference number: Z14248
A:Accession: T01078
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1111 <RAP>
A:Cross-references: EMBL:AC002330; NID:q2262135; PID:g3892059
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4
A:Insertions: 35/1; 795/3
A:Note: T10P11.2.2

Query Match 60.3%; Score 44; DB 2; Length 1111;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WMKDHNTHH 8
||| ||| ||
Db 15 WMDSHNT 22

RESULT 10
A33417
folate-binding protein precursor, placental - human
C:Species: Homo sapiens (man)
C>Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 13-Aug-1999
C:Accession: A53315; A33417; A60442
R:Sadasivan, E.; Cedeno, M.M.; Rothenberg, S.P.
J. Biol. Chem. 269, 4725-4735, 1994
A:Title: Characterization of the gene encoding a folate-binding protein expressed in
Olf for the ets encoded GA-binding protein.
A:Reference number: A53315; MUID:94148914
A:Accession: A53315
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-255 <SAD>
A:Cross-references: GB:U02714
R:Ratnam, M.; Marquardt, H.; Duhring, J.L.; Freilshelm, J.H.
Biochemistry 28, 8249-8254, 1989
A:Title: Homologous membrane folate binding proteins in human placenta: cloning and s
A:Reference number: A33417; MUID:90105335
A:Accession: A33417
A:Molecule type: mRNA
A:Residues: 1-255 <RAV>
A:Cross-references: GB:U02876; NID:g182413; PIDN:AAA3821.1; PID:g182414
R:Freilshelm, J.H.; Price, E.M.; Ratnam, M.
Adv. Enzyme Regul. 29, 13-26, 1989
A:Title: Folate coenzyme and antifolate transport proteins in normal and neoplastic c
A:Reference number: A60442; MUID:90224692
A:Accession: A60442
A:Molecule type: protein
A:Residues: 68-87; 'V', 104-110, 'VR', 113-114, 'D', 116, 'X', 118-121; 174-184 <FRE>
C:Superfamily: folate-binding protein
F:1-21/Domain: signal sequence #status predicted <IG>

Query Match 58.9%; Score 43; DB 2; Length 255;
Best Local Similarity 55.6%; Pred. No. 9.3;

Matches 5: Conservative 2: Mismatches 2: Indels 0: Gaps 0:
QY 1 WVKDKHNT 9
|:|:|:|:
DB 136 WVEDCHTSH 144

RESULT 11
S43772
phosphatidylcholine desaturase (EC 1.3.1.35) - Anabaena variabilis
N:Alternate names: Delta-12 desaturase; fatty acid desaturase (EC 1.14.99.-) [misidentifi
C:Species: Anabaena variabilis
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C:Accession: S43772
R:Sakamoto, T.; Wada, H.; Nishida, I.; Ohmori, M.; Murata, N.
Plant Mol. Biol. 24, 643-650, 1994
A:Title: Identification of conserved domains in the Delta-12 desaturases of cyanobacteri
A:Reference number: S43770; MUID:94207189
A:Accession: S43772
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-350 <SAK>
A:Cross-references: GB:DJ4581; NID:q493223; PIDN:BA03435.1; PID:q493225
C:Superfamily: omega-3 fatty acid desaturase
C:Keywords: oxidoreductase

Query Match 58.9%; Score 43; DB 2; Length 350;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6: Conservative 1: Mismatches 2: Indels 0: Gaps 0:

QY 2 WVKDKHNT 10
|:|:|:|:
DB 118 WRKKNHHH 126

RESULT 12
T42087
probable 6-phosphofructokinase (EC 2.7.1.11) - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: T42087
R:Itohloka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A:Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A:Reference number: Z17323; MUID:96162722
A:Accession: T42087
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-359 <YOS>
A:Cross-references: EMBL:DB9110; NID:q1749427; PIDN:BAA13773.1; PID:q1749428
A:Experimental source: strain PR745
C:Superfamily: human 6-phosphofructokinase; 6-phosphofructokinase 1 homology
C:Keywords: ATP; glycolysis; phosphotransferase

Query Match 58.9%; Score 43; DB 2; Length 359;
Best Local Similarity 71.4%; Pred. No. 13;
Matches 5: Conservative 1: Mismatches 1: Indels 0: Gaps 0:

QY 1 WVKDKHNT 7
|:|:|:|:
DB 341 WVRDMHN 347

RESULT 13
JC5891
omega 6 desaturase (EC 1.14.99.-) precursor, chloroplast - Chlamydomonas reinhardtii
C:Species: Chlamydomonas reinhardtii
C:Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 20-Jun-2000
C:Accession: JC5891
R:Sato, N.; Fujiwara, S.; Kawaguchi, A.; Tsuzuki, M.
J. Biochem. 122, 1224-1232, 1997

A:Title: Cloning of a gene for chloroplast omega 6 desaturase of a green alga, Chlamy
A:Reference number: JC5891; MUID:96158334
A:Accession: JC5891
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-424 <SAT>
A:Cross-references: DBJ:AB007640; NID:q2696716; PIDN:BAA23881.1; PID:q2696717
C:Comment: This enzyme catalyzes the desaturation of monoenolic to dienolic acids.
C:Genetics:

A:Gene: des6
C:Superfamily: omega-3 fatty acid desaturase
C:Keywords: chloroplast; oxidoreductase
F:1-40/Domain: transit peptide (chloroplast) #status predicted <TPS>

Query Match 58.9%; Score 43; DB 2; Length 424;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6: Conservative 1: Mismatches 2: Indels 0: Gaps 0:

QY 2 WVKDKHNT 10
|:|:|:|:
DB 178 WRKKNHHH 186

RESULT 14
T13155
linoleoyl-CoA desaturase (EC 1.14.99.25) [validated] - human
N:Alternate names: Delta6 fatty acid desaturase; protein DKFZp586C201.1
C:Species: Homo sapiens (man)
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jun-2000
C:Accession: T13155; T08765
R:Cho, H.P.; Nakamura, M.T.; Clarke, S.D.
J. Biol. Chem. 274, 471-477, 1999
A:Title: Cloning, expression, and nutritional regulation of the mammalian Delta-6 des
A:Reference number: Z17612; MUID:99085046
A:Accession: T13155
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-444 <CHO>
A:Cross-references: EMBL:AF126799; NID:q4406527; PID:q4406528; PIDN:AA020018.1
R:Wandult, R.; Heudner, D.; Mewes, H.W.; Gassenhuber, J.; Wilmann, S.
submitted to the Protein Sequence Database, March 1999
A:Reference number: Z16471
A:Accession: T08765
A:Molecule type: mRNA
A:Residues: 'RTRG', 138-428, 'D', 430, 'W', 432-444 <MAN>
A:Cross-references: EMBL:AL050118
A:Experimental source: adult uterus; clone DKFZp586C201
C:Genetics:

A:Gene: GDB:FADS6
A:Cross-references: GDB:9956652
A:Note: DKFZp586C201.1
C:Superfamily: cytochrome b5 core homology
C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase; unsaturated fa
F:18-94/Domain: cytochrome b5 core homology <CB5>
F:53,76/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 58.9%; Score 43; DB 2; Length 444;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 5: Conservative 1: Mismatches 4: Indels 0: Gaps 0:

QY 1 WVKDKHNT 10
|:|:|:|:
DB 212 WNNHRHPOH 221

RESULT 15
JC0180
Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
C:Accession: JC0180

R:AKI, T.; Shimada, Y.; Inagaki, K.; Higashimoto, H.; Kawamoto, S.; Shigeta, S.; Ono, K.
 Biochem. Biophys. Res. Commun. 255, 575-579, 1999.
 A:Title: Molecular cloning and functional characterization of rat delta-6 fatty acid des
 A:Reference number: JG0180; MUID:99160394
 A:Accession: JG0180
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-444 <AKI>
 A:Cross-references: DDBJ:AB021980; NID:94514721; PIDN:BA075496.1; PID:94514722
 C:Superfamily: cytochrome b5 core homology
 C:Keywords: heme; iron; metalloprotein; oxidoreductase; unsaturated fatty acid biosynthe
 F:18-94/Domain: cytochrome b5 core homology <CB5>
 F:33,76/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 58.9%; Score 43; DB 2; Length 444;
 Best Local Similarity 50.0%; Pred. No. 17;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WMKDKHNTTH 10
 || : | ||
 Db 212 WMNHRHFQHH 221

Search completed: August 9, 2001, 20:26:07
 Job time: 246 sec

CC -1- SIMILARITY: BELONGS TO THE FOLATE RECEPTOR FAMILY.
 CC -----
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 CC -----
 CC EMBL: X69516; CAA94267.1; -
 CC EMBL: J02876; AAA35821.1; -
 CC EMBL: U02714; AAA17370.1; -
 CC EMBL: U02716; AAA17370.1; JOINED.
 CC PIR: A33417; A33417.
 CC MIM: 136425; -
 CC Receptor; Glycoprotein; Signal; Placenta; Folate-binding; Membrane;
 CC GPI-anchor; Multigene family.
 CC SIGNAL 1 16
 CC CHAIN 17 230 FOLATE RECEPTOR BETA.
 CC PROPEP 231 255 REMOVED IN MATURE FORM.
 CC LIPID 230 230 GPI-ANCHOR.
 CC CARBOHD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CONFLICT 117 117 T -> S (IN REF. 1).
 CC CONFLICT 141 141 H -> L (IN REF. 3).
 CC CONFLICT 244 244 S -> R (IN REF. 3).
 CC SEQUENCE 255 AA; 29293 MW; F0852287A3B81C98 CRC64;
 SO
 Query Match 58.9%; Score 43; DB 1; Length 255;
 Best Local Similarity 55.6%; Pred. No. 5.4;
 ~ Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 WNKDKHNT 9
 Db 136 WMECHTSH 144
 ||:|:|:|
 ACOL_2
 ACOL_YEAST STANDARD; PRT; 510 AA.
 ID ACOL_YEAST PRT; 510 AA.
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE ACYL-COA DESATURASE 1 (EC 1.14.99.5) (STEAROYL-COA DESATURASE 1)
 DE (FATTY ACID DESATURASE 1).
 GN OLE1 OR YGL055W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RX MEDLINE=91056050; PubMed=1978720;
 RA Stucky J.E., McDonough V.M., Martin C.E.;
 RT "The OLE1 gene of Saccharomyces cerevisiae encodes the delta 9 fatty
 RT acid desaturase and can be functionally replaced by the rat stearyl-
 RT COA desaturase gene."
 RL J. Biol. Chem. 265:20144-20149(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=97377993; PubMed=9234674;
 RX Feuerhann M., de Montigny J., Potier S., Souciet J.-L.;
 RA "The characterization of two new clusters of duplicated genes
 RA suggests a 'leugo' organization of the yeast Saccharomyces cerevisiae
 RA chromosomes."
 RL Yeast 13:861-869(1997).
 CC -1- FUNCTION: UTILIZES O(2) AND ELECTRONS FROM THE REDUCED CYTOCHROME
 CC B(5) DOMAIN TO CATALYZE THE INSERTION OF A DOUBLE BOND INTO A
 CC SPECTRUM OF FATTY ACYL-COA SUBSTRATES (PROBABLE).

CC -1- CATALYTIC ACTIVITY: STEAROYL-COA + AH(2) + O(2) -> OLEOYL-COA + A
 CC + 2 H(2)O.
 CC -1- COFACTOR: IRON.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC
 CC RETICULUM (PROBABLE).
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
 CC -1- SIMILARITY: CONTRAINS A CYTOCHROME B5 FAMILY, HEME-BINDING DOMAIN.
 CC -----
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 CC -----
 CC EMBL: J05676; AAA34826.1; -
 CC EMBL: Z72577; CAA96757.1; -
 CC PIR: A23675; A23675.
 CC SGD: S0003023; OLE1.
 CC InterPro: IPR001522; -
 CC Pfam: PF01069; Desaturase; 1.
 CC Pfam: PF00173; heme_1; 1.
 CC PRINTS: PR00075; FACDSATURASE.
 CC PROSITE: PS00191; CYTOCHROME B5_1; 1.
 CC PROSITE: PS50255; CYTOCHROME B5_2; 1.
 CC PROSITE: PS00476; FATTY_ACID_DESATUR_1; 1.
 CC OXidoreductase; Fatty acid biosynthesis; Iron; Electron transport;
 CC Transmembrane; Endoplasmic reticulum; Heme.
 CC TRANSMEM 113 133 POTENTIAL.
 CC TRANSMEM 139 159 POTENTIAL.
 CC TRANSMEM 256 276 POTENTIAL.
 CC TRANSMEM 281 301 POTENTIAL.
 CC DOMAIN 161 166 HISTIDINE BOX 1.
 CC DOMAIN 198 202 HISTIDINE BOX 2.
 CC DOMAIN 335 339 HISTIDINE BOX 3.
 CC DOMAIN 409 487 HEME-BINDING.
 CC BINDING 444 444 HEME LIGAND (BY SIMILARITY).
 CC BINDING 470 470 HEME LIGAND (BY SIMILARITY).
 CC CONFLICT 304 304 L -> M (IN REF. 1).
 CC SEQUENCE 510 AA; 58403 MW; A6CC78DDA210BCCA CRC64;
 SO
 Query Match 57.5%; Score 42; DB 1; Length 510;
 Best Local Similarity 50.0%; Pred. No. 16;
 ~ Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 WNKDKHNT 10
 Db 193 WNGSHRHH 202
 ||:|:|:|
 PSS_3
 PSS_ECOLI STANDARD; PRT; 451 AA.
 ID PSS_ECOLI PRT; 451 AA.
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE CDP-DIACYLGLYCEROL--SERINE O-PHOSPHATIDYLTRANSFERASE (EC 2.7.8.8)
 DE (PHOSPHATIDYL-SERINE SYNTHASE).
 GN PSSA OR PSS.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-12.
 RX MEDLINE=91161632; PubMed=2002065;
 RA Dechavigny A., Heacock P.N., Dowhan W.;
 RT "Sequence and inactivation of the pss gene of Escherichia coli."

RT Phosphatidylethanolamine may not be essential for cell viability."
 RL J. Biol. Chem. 266:5323-5332(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9276503;
 RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 MAU B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12."
 RL Science 277:1453-1474(1997).
 RN [3]
 RP REVIEW.
 RX MEDLINE=92356873; PubMed=1323044;
 RA Dowhan W.;
 RT "Phosphatidylserine synthase from *Escherichia coli*."
 RL Meth. Enzymol. 209:287-298(1992).
 CC -1- CATALYTIC ACTIVITY: CDP-DIACYLGLYCEROL + L-SERINE = CMP + O-SN-
 CC PHOSPHATIDYL-L-SERINE.
 CC -1- SUBUNIT: MULTIMERIC.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC; POSSIBLE INTERACTION WITH THE
 CC INNER MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE CDP-ALCOHOL PHOSPHATIDYLTRANSFERASE
 CC CLASS-II FAMILY.
 CC -----
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 CC -----
 DR EMBL; M58699; AAA97504.1; -
 DR EMBL; AE000345; AAC75638.1; ALT_INIT.
 DR PIR; JH0368; JH0368.
 DR EcoGene; EG10781; PSSA.
 DR InterPro; IPR001736; -
 DR Pfam; PF00614; PLDC_2.
 KW Transferase; Phospholipid biosynthesis; Membrane.
 FT DOMAIN 4
 FT 119 154 LYS-RICH (BASIC).
 FT DOMAIN 239 284 HYDROPHOBIC.
 FT DOMAIN 430 449 ARG/LYS-RICH (BASIC).
 FT CONFLICT 32 32 A -> R (IN REF. 1).
 FT CONFLICT 78 78 R -> DD (IN REF. 1).
 FT CONFLICT 165 167 K YR -> NIA (IN REF. 1).
 FT CONFLICT 287 288 LL -> FV (IN REF. 1).
 FT CONFLICT 309 309 P -> S (IN REF. 1).
 SO SEQUENCE 451 AA; 52801 MW; 9E9A2A5C4B4C814F CRC64;

Query Match 56.2%; Score 41; DB 1; Length 451;
 Best Local Similarity 66.7%; Pred. No. 20;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 WKDKNTHH 10
 DB 349 WKDDNTHH 357

RESULT 4
 AURL_YEAST STANDARD; PRT; 401 AA.
 AC P36107; G92324;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE AUREOBASIDIN A RESISTANCE PROTEIN.
 GN AURL OR YKL004W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 RN NCBI_TaxID=4932;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A89-4A;
 RX MEDLINE=96242157; PubMed=8668135;
 RA Hashida-Okado T., Ogawa A., Endo M., Yasumoto R., Takesako K.,
 RA Kato I.;
 RT "AURL", a novel gene conferring aureobasidin resistance on
 RT Saccharomycetes cerevisiae: a study of defective morphologies in
 RT Aurlp-depleted cells."
 RL Mol. Gen. Genet. 251:236-244(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Boyer J., Pascolo S., Richard G.F., Ghazvini M., Colleaux L.,
 RA Thierry A., Monier A.L., Dujon B.;
 RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ESSENTIAL FOR GROWTH, WILD TYPE PRODUCT IS THE TARGET
 CC FOR AUREOBASIDIN A (ABA). MAY HAVE A ROLE IN MICROTUBULE
 CC ORGANIZATION IN CYTOSKELETON ASSEMBLIES.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE AURL FAMILY.
 CC -----
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 CC -----
 DR EMBL; U49090; AAB06940.1; -
 DR EMBL; Z28004; CAA81836.1; -
 DR PIR; S37815; S37815.
 DR SGD; S0001487; AURL.
 KW Transmembrane.
 FT TRANSMEM 48 68 POTENTIAL.
 FT TRANSMEM 70 90 POTENTIAL.
 FT TRANSMEM 151 171 POTENTIAL.
 FT TRANSMEM 277 297 POTENTIAL.
 FT VARIANT 158 158 F -> Y (IN AURL-1; ABA RESISTANT).
 SO SEQUENCE 401 AA; 45193 MW; 997F92318DF656A7 CRC64;

Query Match 54.8%; Score 40; DB 1; Length 401;
 Best Local Similarity 50.0%; Pred. No. 25;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 WKDKNTHH 10
 DB 285 WKSTMYLTHH 294

RESULT 5
 AURL_CANAL STANDARD; PRT; 471 AA.
 ID AURL_CANAL
 AC O13332;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE AUREOBASIDIN A RESISTANCE PROTEIN HOMOLOG.
 GN AURL.
 OS Candida albicans (Yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=5476;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TIMM 0136;
 RA Kondo A., Hashida-Okado T., Takesako K., Kato I.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE AURL FAMILY.

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CC -----
DR EMBL: AF013799; AAB67233.1; -
KM Transmembrane.
FT TRANSMEM 61 81 POTENTIAL.
FT TRANSMEM 83 103 POTENTIAL.
FT TRANSMEM 105 125 POTENTIAL.
FT TRANSMEM 164 184 POTENTIAL.
FT TRANSMEM 193 213 POTENTIAL.
FT TRANSMEM 259 279 POTENTIAL.
SQ SEQUENCE 471 AA; 53475 MW; C9C01509C86C1B46 CRC64;

Query Match
Best Local Similarity 54.8%; Score 40; DB 1; Length 471;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 WVKDKNTHH 10
   1 111
Db 298 WNSTWYLTTH 307

RESULT 6
PDB_CORPUS STANDARD; PRT; 307 AA.
AC P20626; Q59314;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PHOSPHOLIPASE D PRECURSOR (EC 3.1.4.4) (PLD) (CHOLINE PHOSPHATASE).
GN PLD.
OS Corynebacterium pseudotuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Corynebacteriaceae;
OC Corynebacterium.
OX NCBI_TaxID=1719;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 25-47.
RA Hoggson A.L.M., Bird P., Nisbet I.T.;
RT "Cloning, nucleotide sequence, and expression in Escherichia coli of
RT the phospholipase D gene from Corynebacterium pseudotuberculosis.";
RL J. Bacteriol. 172:1256-1261(1990).
RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN-BIOVAR OVIS / ISOLATE WHETTEN 1;
RX MEDLINE-90093451; PubMed-2403529;
RA Songer J.G., Libby S.J., Iandolo J.J., Cuevas W.A.;
RT "Cloning and expression of the phospholipase D gene from
RT Corynebacterium pseudotuberculosis in Escherichia coli.";
RL Infect. Immun. 58:131-136(1990).
RN [3]
RP SEQUENCE FROM N.A.
RP STRAIN-BIOVAR EQUI / ISOLATE 155;
RX MEDLINE-95255653; PubMed-7737503;
RA McNamara P.J., Cuevas W.A., Songer J.G.;
RT "Toxic phospholipases D of Corynebacterium pseudotuberculosis, C.
RT ulcerans and Arcanobacterium haemolyticum: Cloning and sequence
RT homology.";
RL Gene 156:113-118(1995).
RN [4]
RP MUTAGENESIS.
RP STRAIN-BIOVAR OVIS / ISOLATE WHETTEN 1;
RX MEDLINE-95020614; PubMed-7934899;
RA McNamara P.J., Bradley G.A., Songer J.G.;
RT "Targeted mutagenesis of the phospholipase D gene results in

```

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RT decreased virulence of Corynebacterium pseudotuberculosis.";
RL Mol. Microbiol. 12:921-930(1994).
CC -1- FUNCTION: VIRULENCE FACTOR AFFECTING BACTERIAL DISSEMINATION AND
CC SURVIVAL WITHIN THE HOST. HAS MAGNESIUM-DEPENDENT SPHINGOMYELINASE
CC AND HEMOLYTIC ACTIVITY.
CC -1- CATALYTIC ACTIVITY: A PHOSPHATIDYLCHOLINE + H(2)O = CHOLINE + A
CC PHOSPHATIDATE.
CC -1- SIMILARITY: TO OTHER CORYNEBACTERIUM PHOSPHOLIPASES D.
CC -----
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CC -----
DR EMBL: L16587; AAA64910.1; -
DR EMBL: L16586; AAA99867.1; -
DR PIR: A35125; A35125.
KM Hydrolase; Lipid degradation; Magnesium; Virulence; Signal.
FT SIGNAL 1 24
FT CHAIN 25 307
FT ACT_SITE 44 44 PHOSPHOLIPASE D.
FT VARIANT 5 6 POTENTIAL.
FT VARIANT 8 8 VV -> FA (IN BIOVAR EQUI / ISOLATE 155).
FT VARIANT 189 189 F -> L (IN BIOVAR EQUI / ISOLATE 155).
FT VARIANT 205 205 E -> G (IN BIOVAR EQUI / ISOLATE 155).
FT VARIANT 270 270 N -> D (IN BIOVAR EQUI / ISOLATE 155).
FT VARIANT 277 277 I -> M (IN BIOVAR EQUI / ISOLATE 155).
FT VARIANT 277 277 A -> P (IN BIOVAR EQUI / ISOLATE 155).
SQ SEQUENCE 307 AA; 33884 MW; D3B1334EFC99875 CRC64;

Query Match
Best Local Similarity 54.1%; Score 39.5; DB 1; Length 307;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

OY 2 WVKDKNTHH 10
   1 111
Db 289 WVDKSHATTH 298

RESULT 7
PDB_CORPUS STANDARD; PRT; 307 AA.
AC Q59332;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PHOSPHOLIPASE D PRECURSOR (EC 3.1.4.4) (CHOLINE PHOSPHATASE).
GN PLD.
OS Corynebacterium ulcerans.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Corynebacteriaceae;
OC Corynebacterium.
OX NCBI_TaxID=65058;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN-ATCC 739;
RX MEDLINE-95255653; PubMed-7737503;
RA McNamara P.J., Cuevas W.A., Songer J.G.;
RT "Toxic phospholipases D of Corynebacterium pseudotuberculosis, C.
RT ulcerans and Arcanobacterium haemolyticum: Cloning and sequence
RT homology.";
RL Gene 156:113-118(1995).
CC -1- FUNCTION: HAS SPHINGOMYELINASE AND HEMOLYTIC ACTIVITY. THOUGHT TO
CC ACT AS A VIRULENCE FACTOR.
CC -1- CATALYTIC ACTIVITY: A PHOSPHATIDYLCHOLINE + H(2)O = CHOLINE + A
CC PHOSPHATIDATE.
CC -1- SIMILARITY: TO OTHER CORYNEBACTERIUM PHOSPHOLIPASES D.
CC -----
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MMNSTNKL SVIIPLYNAGDDFRJCMC -> MRAMISALVWK
(IN REF. 2).

SEQUENCE FROM N.A.

RA Lu M., Iatrou K.;
RT "Characterization of a domain of the genome of BMNV containing a
functional gene for a small capsid protein and harboring deletions
eliminating three open reading frames that are present in AcNPV.";
RL Gene 185:69-75(1997).
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CC -----
DR EMBL; U55072; AAC56599.1; -
KW Coat protein.
SQ SEQUENCE 126 AA; 15038 MW; A925730D51EB65A CRC64;

QY 2 WKDKNTHH 10
11:1111
DB 79 WRDTNNWHH 87

Query Match 53.4%; Score 39; DB 1; Length 126;
Best Local Similarity 55.6%; Pred. No. 11;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 11
IS12_STRAL STANDARD; PRT; 256 AA.
ID IS12_STRAL
AC P23393;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1991 (Rel. 20, Last annotation update)
DE INSERTION ELEMENT IS112 28.4 KDA PROTEIN.
OS Streptomyces albus G.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycetales; Streptomycetaceae; Streptomyces.
OX NCBI_TaxId=1962;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-91155926; PubMed-1947988;
RA Rodicio M.R., Alvarez M.A., Chater K.F.;
RT "Isolation and genetic structure of IS112, an insertion sequence
RT responsible for the inactivation of the SalI restriction-modification
RT system of Streptomyces albus G.";
RL Mol. Gen. Genet. 225:142-147(1991).
CC -1- FUNCTION: INACTIVATION OF SAL I RESTRICTION-MODIFICATION SYSTEM.
CC -----
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CC -----
DR EMBL; X56644; CA39965.1; -
KW Transposable element.
SQ SEQUENCE 256 AA; 28409 MW; 8BFA8FE16DC918E7 CRC64;

QY 2 WKDKNTHH 10
11:1111
DB 201 WKEHNKSH 209

Query Match 53.4%; Score 39; DB 1; Length 256;
Best Local Similarity 55.6%; Pred. No. 22;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 12

FD31_BRANA STANDARD; PRT; 377 AA.
ID FD31_BRANA
AC P46311;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
DE (VERSION 1).
GN FAD3.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxId=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed.
RX MEDLINE-94302147; PubMed-8029334;
RA Yadav N.S., Wierzbicki A., Aegerter M., Caster C.S., Perez-Grau L.,
RA Kinney A.J., Hiltz W.D., Booth J.R., Jr., Schweizer B., Stecca K.L.,
RA Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H.,
RA Feldmann K.A., Pierce J., Browne J.,
RT "Cloning of higher plant omega-3 fatty acid desaturases.";
RL Plant Physiol. 103:467-476(1993).
CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC CYCLOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L22962; AAA61775.1; -
DR InterPro; IPR001225; -
DR Pfam; PF00487; FA_desaturase; 1.
KW Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
KW Transmembrane.
KW TRANSMEM 54 73
FT TRANSMEM 203 226 POTENTIAL.
FT TRANSMEM 233 251 POTENTIAL.
FT DOMAIN 92 96 HISTIDINE BOX 1.
FT DOMAIN 128 132 HISTIDINE BOX 2.
FT DOMAIN 295 299 HISTIDINE BOX 3.
SQ SEQUENCE 377 AA; 43258 MW; 723BD457212F2FC0 CRC64;

QY 2 WKDKNTHH 10
11:1111
DB 124 WRISHRTHH 132

Query Match 53.4%; Score 39; DB 1; Length 377;
Best Local Similarity 55.6%; Pred. No. 33;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

RESULT 13
FD3E_TOBAC STANDARD; PRT; 379 AA.
ID FD3E_TOBAC
AC P48626;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 01-OCT-1996 (Rel. 34, last annotation update)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-).
GN FAD3.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta;
OC Magnoliophyta: eudicotyledons: core eudicots: Asteridae: euasterids I;
OC Solanales: Solanaceae: Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. SRI:TISSUE-Leaf.
RA MEDLINE-95011632; Pubmed-7926817;
RA Hamada T., Kodama H., Nishimura M., Iba K.;
RT "Cloning of a cDNA encoding tobacco omega-3 fatty acid desaturase";
RL Gene 147:293-294(1994).
CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D26509; BAA05515.1; -.
DR InterPro: IPR001225; -.
DR Pfam: PF00487; FA_desaturase; 1.
KM Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
KM Transmembrane.
FT TRANSMEM 52 72 POTENTIAL.
FT TRANSMEM 213 233 POTENTIAL.
FT TRANSMEM 236 256 POTENTIAL.
FT DOMAIN 97 101 HISTIDINE BOX 1.
FT DOMAIN 133 137 HISTIDINE BOX 2.
FT DOMAIN 300 304 HISTIDINE BOX 3.
SQ SEQUENCE 379 AA; 44149 MW; 87221A21AB02E1B2 CRC64;

Query Match 53.4%; Score 39; DB 1; Length 379;
Best Local Similarity 55.6%; Pred. No. 33;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 WKDKHNTTH 10
I: | | | |
Db 129 WRISHKTHH 137

RESULT 14
FD3E_PHAU STANDARD; PRT; 380 AA.
ID FD3E_PHAU
AC P32291;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
DE (INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG1).
GN ARG1.
OS Phaseolus aureus (Mung bean) (Vigna radiata).
OC Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta;
OC Magnoliophyta: eudicotyledons: core eudicots: Rosidae: eurosids I;
OC Fabales: Fabaceae: Papilionoideae; Vigna.
OX NCBI_TaxID=3916;

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Hypocotyl;
RA Yamamoto K.T., Mori H., Imaseki H.;
RT "Novel mRNA sequences induced by indole-3-acetic acid in sections of
RT elongating hypocotyls of mung bean (Vigna radiata)".
RL Plant Cell Physiol. 33:13-20(1992).
CC -1- FUNCTION: MICROSOAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- INDUCTION: BY AUXIN, ETHYLENE AND WOUNDING.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D14410; BAA03306.1; -.
DR InterPro: IPR001225; -.
DR Pfam: PF00487; FA_desaturase; 1.
KM Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
KM Transmembrane.
FT TRANSMEM 59 78 POTENTIAL.
FT TRANSMEM 208 231 POTENTIAL.
FT TRANSMEM 236 256 POTENTIAL.
FT DOMAIN 97 101 HISTIDINE BOX 1.
FT DOMAIN 133 137 HISTIDINE BOX 2.
FT DOMAIN 300 304 HISTIDINE BOX 3.
SQ SEQUENCE 380 AA; 43996 MW; 1C005117A8DAE16B CRC64;

Query Match 53.4%; Score 39; DB 1; Length 380;
Best Local Similarity 55.6%; Pred. No. 34;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 WKDKHNTTH 10
I: | | | |
Db 129 WRISHKTHH 137

RESULT 15
FD3E_SOYBN STANDARD; PRT; 380 AA.
ID FD3E_SOYBN
AC P48625;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-).
DE FAD3.
GN Glycine max (Soybean).
OC Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta;
OC Magnoliophyta: eudicotyledons: core eudicots: Rosidae: eurosids I;
OC Fabales: Fabaceae: Papilionoideae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Seed;
RA MEDLINE-94302147; Pubmed-8029334;
RA Yedav N.S., Wierzbicki A., Aegerter M., Caster C.S., Perez-Grau L.,
RA Kinney A.J., Hiltz W.D., Booth J.R., Schweiger B., Stecca K.L.,
RA Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H.,
RA Feldmann K.A., Pierce J., Browne J.;

```

RT "Cloning of higher plant omega-3 fatty acid desaturases.";
RL Plant Physiol. 103:467-476(1993).
CC -! FUNCTION: MICROSOMAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -! PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -! SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -! DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -! SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L22964; AAA61777.1; -.
DR PIR: JQ2338; JQ2338.
DR InterPro: IPR001225; -.
DR Pfam: PF00487; FA_desaturase; 1.
KW Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
KW Transmembrane.
FT TRANSMEM 55 75 POTENTIAL.
FT TRANSMEM 212 232 POTENTIAL.
FT TRANSMEM 236 256 POTENTIAL.
FT DOMAIN 100 104 HISTIDINE BOX 1.
FT DOMAIN 136 140 HISTIDINE BOX 2.
FT DOMAIN 303 307 HISTIDINE BOX 3.
SQ SEQUENCE 380 AA: 44185 MW; BF600F93CF4C29D7 CRC64;

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Query Match          53.4%; Score 39; DB 1; Length 380;
Best Local Similarity 55.6%; Pred. No. 34;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY 2 WKDKNHTHH 10
   1: | | | |
Db 132 WRISHRTHH 140

```

```

Search completed: August 9, 2001, 20:36:51
Job time: 700 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 9, 2001, 20:36:17 ; Search time 87.05 Seconds
(without alignments)
15.199 Million cell updates/sec

Title: US-09-367-013b-2_COPY_204_213

Sequence: 1 WMKDKHNTHH 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_16:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp-organella:*
10: sp-phage:*
11: sp-plant:*
12: sp-rodent:*
13: sp-unclassified:*
14: sp-vertebrate:*
15: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	73	100.0	357	3	09HDF4
2	73	100.0	443	5	061388
3	73	100.0	443	5	023221
4	73	100.0	457	3	09UVY3
5	73	100.0	457	3	09UVY3
6	73	100.0	457	3	09HEV4
7	73	100.0	457	3	09HEV1
8	63	86.3	523	3	09HDG8
9	63	86.3	525	10	09ZNM2
10	62	84.9	350	2	09F2M3
11	60	82.2	520	10	09LEW9
12	59	80.8	469	10	09ZTU8
13	58	79.5	446	10	09ZTY9
14	57	78.1	345	2	09XBM4
15	57	78.1	483	10	09LENO
16	54	74.0	419	10	09SMO9
17	53	72.6	448	10	09SAU5
18	53	72.6	448	10	09SAU5
19	52	71.2	446	10	09ZT29

20	52	71.2	446	10	09FR82	09f82 borago offi
21	52	71.2	449	10	082348	082348 arabidopsis
22	52	71.2	449	10	09ZRP8	09zrp8 brassica na
23	52	71.2	449	10	09ZRP7	09zrp7 arabidopsis
24	52	71.2	458	10	043469	043469 bellanthus
25	51	69.9	676	5	09NGL5	09ngl5 callinectes
26	50	68.5	347	2	09FC35	09fc35 streptomyce
27	50	68.5	650	5	023707	023707 cancer magi
28	49	67.1	447	5	09XR87	09xrt7 caenorhabdi
29	47	64.4	300	2	09R6T6	09r6t6 synchococc
30	45	61.6	182	3	P79067	P79067 yarrowia ll
31	44	60.3	348	10	09FPA4	09fpa4 oryza sativ
32	44	60.3	352	2	09LA14	09la14 gloeobacter
33	44	60.3	111	10	09ZOX8	09zox8 arabidopsis
34	43	58.9	204	3	09U024	09u024 schizosacch
35	43	58.9	311	4	09Y3X4	09y3x4 homo sapien
36	43	58.9	350	2	044503	044503 anabaena va
37	43	58.9	359	3	P78762	P78762 schizosacch
38	43	58.9	407	5	09VG54	09vg54 drosophila
39	43	58.9	421	10	09SBU4	09sbu4 chlamydomon
40	43	58.9	422	4	09H3G3	09h3g3 homo sapien
41	43	58.9	424	10	048663	048663 chlamydomon
42	43	58.9	444	4	09S864	09s864 homo sapien
43	43	58.9	444	11	09Z122	09z122 rattus norv
44	43	58.9	444	11	09Z0R9	09z0r9 mus musculu
45	43	58.9	444	13	09DEX7	09dex7 brachydanio

ALIGNMENTS

RESULT 1
ID 09HDF4 PRELIMINARY; PRT; 357 AA.

AC 09HDF4;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE DELTA 6-PATRY ACID DESATURASE (FRAGMENT).
OS Mortierella alpina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae;
OC Mortierella.
OX NCBI_TaxID=64518;
RN [1]
RP SEQUENCE FROM N.A.
RA Xing L., Li M., Liu L., Hu G., Zhang L.;
RT "Cloning and sequence analysis of the conserved region of delta 6-
RT fatty acid desaturase gene from Mortierella alpina.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Xing L., Li M., Liu L., Hu G., Zhang L.;
RT "Cloning and sequence analysis of the conserved region of delta 6-
RT fatty acid desaturase gene from Mortierella alpina.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF307942; AAC45094.1; -;
DR EMBL: AF307941; AAC45093.1; -;
FT NON_TER
FT 357
SQ SEQUENCE 357 AA; 40796 MW; C8D9CE1283B816B8 CRC64;

Query Match 100.0%; Score 73; DB 3; Length 357;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMKDKHNTHH 10
|||||
Db 159 WMKDKHNTHH 168

RESULT 2
061388

```

ID 061388      PRELIMINARY;      PRT;      443 AA.
AC 061388;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE DELTA6-FATTY-ACID-DESATURASE.
OC Caenorhabditis elegans.
OC Rhabditidae; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC NCB1_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268723; PubMed=9108131;
RA Sayanova O., Smith M.A., Lapinskas P., Stobart A.K., Dobson G.,
RA Christie W.W., Shewry P.R., Napier J.A.;
RT "Expression of a borage desaturase cDNA containing an N-terminal
RT cytochrome b5 domain results in the accumulation of high levels of
RT delta6-desaturated fatty acids in transgenic tobacco."
RT Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98149727; PubMed=9480865;
RA Napier J.A., Hey S.T., Lacey D.J., Shewry P.R.;
RT "Identification of a Caenorhabditis elegans Delta6-fatty-acid-
RT desaturase by heterologous expression in Saccharomyces cerevisiae."
RT Biochem. J. 330:0-0(0).
DR EMBL: AF031477; AAC15586.1;
DR InterPro: IPR000566;
DR InterPro: IPR001199;
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
DR PROSITE: PS00213; LIPOCALIN; UNKNOWN_1.
SO SEQUENCE 443 AA; 51740 MW; 9513CA7C5A7E9A06 CRC64;

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Query Match      100.0%; Score 73; DB 5; Length 443;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WMKDKHNTHH 10
DB 200 WMKDKHNTHH 209

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RESULT 3
ID 023221      PRELIMINARY;      PRT;      443 AA.
AC 023221;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE W08D2.4 PROTEIN.
GN W08D2.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCB1_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Swilburne J., Ainscough R.;
RT Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL: 270271; CAA94233.2;
DR InterPro: IPR000566;
DR InterPro: IPR001199;
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
DR PROSITE: PS00213; LIPOCALIN; UNKNOWN_1.
SO SEQUENCE 443 AA; 51772 MW; 9513D611ECB99A06 CRC64;

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```

Query Match      100.0%; Score 73; DB 5; Length 443;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WMKDKHNTHH 10
DB 200 WMKDKHNTHH 209

```

```

RESULT 4
ID 090VV3      PRELIMINARY;      PRT;      457 AA.
AC 090VV3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE DELTA-6 FATTY ACID DESATURASE.
OS Mortierella alpina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae;
OC Mortierella.
OX NCB1_TaxID=64518;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=1S-4;
RX MEDLINE=20035749; PubMed=10570972;
RA Sakurada E., Kobayashi M., Shimizu S.;
RT "Delta 6-Fatty acid desaturase from an arachidonic acid-producing
RT Mortierella fungus. Gene cloning and its heterologous expression in a
RT fungus, Aspergillus."
RT Gene 238:445-453(1999).
CC -I- SIMILARITY: TO CYTOCHROME B5 DOMAIN.
DR EMBL: AB020032; BA85588.1;
DR HSP: P04166; IBSM.
DR InterPro: IPR001199;
DR Pfam: PF00173; heme_1; 1.
DR PROSITE: PS00191; CYTOCHROME_B5_1; UNKNOWN_1.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SO SEQUENCE 457 AA; 51816 MW; 5C4B3D7312439543 CRC64;

```

```

Query Match      100.0%; Score 73; DB 3; Length 457;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WMKDKHNTHH 10
DB 204 WMKDKHNTHH 213

```

```

RESULT 5
ID 090VV3      PRELIMINARY;      PRT;      457 AA.
AC 090VV3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE DELTA-6 FATTY ACID DESATURASE.
OS Mortierella alpina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae;
OC Mortierella.
OX NCB1_TaxID=64518;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC32221;
RX MEDLINE=99406036; PubMed=10478922;
RA Huang Y.S., Chaudhary S., Thurmond J.M., Bobik E.G. Jr., Yuan L.,
RA Chan G.M., Kirchner S.J., Mukerji P., Knutson D.S.;
RT "Cloning of delta12- and delta6-desaturases from Mortierella alpina
RT and recombinant production of gamma-linolenic acid in Saccharomyces
RT cerevisiae."

```

RL Lipids 34:649-659(1999).
 CC -1- SIMILARITY: TO CYTOCHROME B5 DOMAIN.
 DR EMBL: AF110510; AAF08685.1; -
 DR HSSP: P04166; 1B5M.
 DR InterPro: IPR001199; -
 DR Pfam: PF00173; heme_1; 1.
 DR PROSITE: PS00191; CYTOCHROME_B5_1; UNKNOWN_1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 457 AA; 51837 MW; D90169EB6911450A CRC64;

Query Match 100.0%; Score 73; DB 3; Length 457;
 Best Local Similarity 100.0%; Pred. No. 0.00059;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMKDKHNTTH 10
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 DB 204 WMKDKHNTTH 213

RESULT 6
 Q9HEV4 PRELIMINARY; PRT; 457 AA.
 AC Q9HEV4;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE DELTA6-FATTY ACID DESATURASE.
 OS Mortierella isabellina.
 OC Eukaryota; Fungi; Zygomycota; Mucorales; Mortierellaceae;
 OC Mortierella.
 OX NCBI_TaxID=91625;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ming-Chun L., Li L., Guo-Wu H., Li Z., Lai-Jun X.;
 RT "Cloning and sequencing analysis of delta6-fatty acid desaturase gene
 from Mortierella isabellina.";
 RT Junwu Xitong 0:0-0(2001).
 DR EMBL: AF306634; AAC38104.1; -
 SQ SEQUENCE 457 AA; 51772 MW; 8687EB21172D5AF CRC64;

Query Match 100.0%; Score 73; DB 3; Length 457;
 Best Local Similarity 100.0%; Pred. No. 0.00059;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMKDKHNTTH 10
 |||||
 DB 204 WMKDKHNTTH 213

RESULT 7
 Q9HEV1 PRELIMINARY; PRT; 457 AA.
 AC Q9HEV1;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE DELTA 6-FATTY ACID DESATURASE.
 OS Mortierella alpina.
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae;
 OC Mortierella.
 OX NCBI_TaxID=64518;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Xing L., Li M., Liu L., Hu G., Zhang L.;
 RT "Expression of Mortierella alpina delta 6-fatty acid desaturase gene
 in Saccharomyces cerevisiae.";
 RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF307940; AAC45092.1; -
 SQ SEQUENCE 457 AA; 51885 MW; 4B0AC0DD15D190A1 CRC64;

Query Match 100.0%; Score 73; DB 3; Length 457;
 Best Local Similarity 100.0%; Pred. No. 0.00059;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMKDKHNTTH 10
 |||||
 DB 204 WMKDKHNTTH 213

RESULT 8
 Q9HDG8 PRELIMINARY; PRT; 523 AA.
 AC Q9HDG8;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE DELTA-6 DESATURASE.
 OS Mucor rouxii.
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
 OC Mucor.
 OX NCBI_TaxID=29923;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 24905;
 RX MEDLINE=20563795; Pubmed-11112411;
 RA Laoteng K., Mannontarat R., Tanticharoen M., Cheevadhanarak S.;
 RT "delta(6)-desaturase of Mucor rouxii with high similarity to plant
 delta(6)-desaturase and its heterologous expression in Saccharomyces
 cerevisiae.";
 RT Biochem. Biophys. Res. Commun. 279:17-22(2000).
 DR EMBL: AF296076; AAC36960.1; -
 DR EMBL: AF290983; AAC36959.1; -
 SQ SEQUENCE 523 AA; 60622 MW; A03727AF39EB7857 CRC64;

Query Match 86.3%; Score 63; DB 3; Length 523;
 Best Local Similarity 80.0%; Pred. No. 0.025;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WMKDKHNTTH 10
 |||||
 DB 265 WMKDKHNTTH 274

RESULT 9
 Q9ZNM2 PRELIMINARY; PRT; 525 AA.
 ID Q9ZNM2;
 AC Q9ZNM2;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE DELTA6-ACYL-LIPID DESATURASE.
 GN DES6.
 OS Physcomitrella patens (Moss).
 OC Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida;
 OC Funariidae; Funariales; Funariaceae; Physcomitrella.
 OX NCBI_TaxID=3218;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HEDW. B. S. G.;
 RX MEDLINE=98416756; Pubmed-9744093;
 RA Girke T., Schmidt H., Zaehlinger U., Reski R., Heinz E.;
 RT "Identification of a novel delta 6-acyl-group desaturase by targeted
 gene disruption in Physcomitrella patens.";
 RT Plant J. 15:39-48(1998).
 CC -1- SIMILARITY: TO CYTOCHROME B5 DOMAIN.
 DR EMBL: AJ222981; CA11033.1; -
 DR EMBL: AJ222980; CA11032.1; -
 DR HSSP: P04166; 1B5M.
 DR InterPro: IPR001199; -
 DR Pfam: PF00173; heme_1; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.

KW Heme. 525 AA; 59369 MW; 530F158B0C97C83F CRC64;
SQ SEQUENCE

Query Match 86.3%; Score 63; DB 10; Length 525;
Best Local Similarity 80.0%; Pred. No. 0.025;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WVKDKHNTTH 10
||| ||| ||
DB 286 WVKDKHNTTH 295

RESULT 10
O9F2M3 PRELIMINARY; PRT; 350 AA.

AC O9F2M3:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE PUTATIVE FATY ACID DESATURASE.
GN SCH63.05C.

OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Oliver K., Harris D.;
RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.

RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denaplatte D., Eichner A., Cullum J.,
RA Kinash H., Hopwood D.A.;

RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).

DR EMBL: AL442629; CAC10296.1;
SQ SEQUENCE 350 AA; 38678 MW; 240C0BA1F428E5 CRC64;

Query Match 84.9%; Score 62; DB 2; Length 350;
Best Local Similarity 80.0%; Pred. No. 0.024;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 WVKDKHNTTH 10
||| ||| ||
DB 119 WVKDKHNTTH 128

RESULT 11
O9LEM9 PRELIMINARY; PRT; 520 AA.

AC O9LEM9:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE DELTA 6-FATY ACID DESATURASE.

OS Ceratodon purpureus (Moss).
OC Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida;

OC Dicranidae; Dicranales; Dicranaceae; Ceratodon.
OX NCBI_TaxID=3225;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WT3; TISSUE=PROTONEMATA;

RX MEDLINE=20307617; PubMed=10848999;
RA Sperling P., Lee M., Girke T., Zaehring U., Stymne S., Heinz E.;
RT "A bifunctional delta 6-fatty acyl acetylase/desaturase from the
RT moss Ceratodon purpureus. A new member of the cytochrome b5
RT superfamily.";
RL Eur. J. Biochem. 267:3801-3811(2000).

DR EMBL: AJ250735; CAB94993.1;
DR InterPro: IPR001199;
DR Pfam: PF00173; heme_1; 1.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
SQ SEQUENCE 520 AA; 59160 MW; 5A9332ECC153439 CRC64;

Query Match 82.2%; Score 60; DB 10; Length 520;
Best Local Similarity 80.0%; Pred. No. 0.073;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 WVKDKHNTTH 10
||| ||| ||
DB 281 WVKDKHNTTH 290

RESULT 12
O9ZTU8 PRELIMINARY; PRT; 469 AA.

AC O9ZTU8:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE S276.
GN S276.

OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae;
OC Triticum.
OX NCBI_TaxID=4565;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. ET3;
RA Delhaize E., Hebb D.M., Gardner R.C., Richards K.D.;
RT "Aluminum tolerance in yeast conferred by over-expression of wheat
RT genes.";
RL Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.

CC -1- SIMILARITY: TO CYTOCHROME B5 DOMAIN.
DR EMBL: AF031194; AAD10250.1;
DR HSRP: P04166; IAMP.

DR Mendel: 35849; Triae; 2419; 35849.

DR InterPro: IPR001199;

DR InterPro: IPR003015;

DR Pfam: PF00173; heme_1; 1.

DR PRINTS: PR00363; CYTOCHROME_B5.

DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
KW Heme.

Query Match 80.8%; Score 59; DB 10; Length 469;
Best Local Similarity 80.0%; Pred. No. 0.094;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 WVKDKHNTTH 10
||| ||| ||
DB 211 WVKDKHNTTH 220

RESULT 13
O9ZTY9 PRELIMINARY; PRT; 446 AA.

AC O9ZTY9:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE DESATURASE/CYTOCHROME B5 PROTEIN.
 OS Ricinus communis (Castor bean).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 OC Malpighiales; Euphorbiaceae; Ricinus.
 OX NCBI_TaxID=3988;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SPECIFIC ENDOPERME;
 RX MEDLINE=97268723; PubMed=9108131;
 RA Sayanova O., Smith M.A., Lapinskas P., Stobart A.K., Dobson G.,
 RT Christie W.W., Shewry P.R., Napier J.A.;
 RT "Expression of a borage desaturase cDNA containing an N-terminal
 cytochrome b5 domain results in the accumulation of high levels of
 delta6-desaturated fatty acids in transgenic tobacco."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
 CC -1- SIMILARITY: TO CYTOCHROME B5 DOMAIN.
 DR EMBL; AF005096; A001240.1; -.
 DR HSSP; P00171; 1WDB.
 DR Mendel; 35711; Rlcco; 2419; 35711.
 DR InterPro; IPR001199; -.
 DR Pfam; PF00173; heme_1; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 446 AA; 51418 MW; A1954FDB2DDB600F CRC64;
 QY 1 WMDKHNTHH 10
 Db 189 WMDKHNTHH 198
 RESULT 14
 Q9X8W4 PRELIMINARY; PRT; 345 AA.
 AC Q9X8W4;
 DT 01-NOV-1999 (TREMURel. 12, Created)
 DT 01-NOV-1999 (TREMURel. 12, Last sequence update)
 DE PUTATIVE DELTA FATTY ACID DESATURASE.
 GN SCH35.42C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Oliver K., Harris D.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Bentley S.D., Parkhill J., Barrett B.G., Rajandream M.A.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denapate D., Eichner A., Cullum J.,
 RT Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome."
 RL M01. Microbiol. 21:77-96(1996).
 DR EMBL; A1078610; CAB44385.1; -.
 SQ SEQUENCE 345 AA; 38022 MW; 1C938614F662DC3A CRC64;

Query Match 78.1%; Score 57; DB 2; Length 345;
 Best Local Similarity 70.0%; Pred. No. 0.14;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 WMDKHNTHH 10
 Db 114 WMDKHNTHH 123
 RESULT 15
 Q9LENO PRELIMINARY; PRT; 483 AA.
 ID Q9LENO
 AC Q9LENO;
 DT 01-OCT-2000 (TREMURel. 15, Created)
 DT 01-OCT-2000 (TREMURel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMURel. 16, Last annotation update)
 DE DELTA 6-FATTY ACETYLENASE.
 OS Ceratodon purpureus (Moss).
 OC Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida;
 OC Dicranidae; Dicranales; Ditrichaceae; Ceratodon.
 OX NCBI_TaxID=3225;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WT3; TISSUE-PROTONEMATA;
 RX MEDLINE=20307617; PubMed=10848999;
 RA Sperling P., Lee M., Girke T., Zaehring U., Stymer S., Heinz E.;
 RT "A bifunctional delta 6-fatty acyl acetylase/desaturase from the
 moss Ceratodon purpureus. A new member of the cytochrome b5
 superfamily."
 RL Eur. J. Biochem. 267:3801-3811(2000).
 DR EMBL; AJ250734; CAB94892.1; -.
 DR InterPro; IPR001199; -.
 DR Pfam; PF00173; heme_1; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 SQ SEQUENCE 483 AA; 54857 MW; C451D042169ABIC2 CRC64;
 QY 1 WMDKHNTHH 10
 Db 244 WMDKHNTHH 253

Search completed: August 9, 2001, 20:36:18
 Job time: 717 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 9, 2001, 20:24:15 ; Search time 79.24 Seconds
(without alignments)
3.825 Million cell updates/sec

Title: US-09-367-013b-2_COPY_172_176

Perfect score: 32
Sequence: 1 HDPLH 5

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	331	21	Arabidopsis thaliana
2	32	100.0	351	21	Arabidopsis thaliana
3	32	100.0	355	19	Desaturase enzyme
4	32	100.0	373	21	Arabidopsis thaliana
5	32	100.0	457	19	AAW84137
6	32	100.0	457	20	AAW95504
7	32	100.0	457	20	AAW85121
8	32	100.0	457	21	AAW92599
9	32	100.0	457	21	AAW56045
10	32	100.0	457	22	AAW31684
11	32	100.0	483	22	AAW46435

12	32	100.0	483	22	AAW46436
13	32	100.0	520	22	AAW46440
14	32	100.0	525	21	AAW51354
15	32	100.0	525	22	AAW46810
16	32	100.0	582	17	AAW95601
17	32	100.0	701	21	AAW39667
18	32	100.0	705	21	AAW39666
19	32	100.0	742	21	AAW39665
20	30	93.8	130	21	AAW37863
21	29	90.6	294	19	AAW76413
22	29	90.6	986	13	AAW25141
23	29	90.6	1129	16	AAW70830
24	29	90.6	1129	20	AAW21699
25	29	90.6	1129	21	AAW35719
26	29	90.6	1132	20	AAW21698
27	29	90.6	1132	21	AAW77552
28	29	90.6	1139	19	AAW76425
29	28	87.5	24	11	AAW08083
30	28	87.5	142	21	AAW40971
31	28	87.5	158	17	AAW97225
32	28	87.5	158	21	AAW10820
33	28	87.5	195	17	AAW97229
34	28	87.5	240	21	AAW09118
35	28	87.5	392	21	AAW09117
36	28	87.5	406	21	AAW09116
37	28	87.5	437	21	AAW17990
38	28	87.5	441	21	AAW17989
39	28	87.5	889	22	AAW68848
40	28	87.5	1956	22	AAW61996
41	28	87.5	1962	20	AAW17250
42	28	87.5	1980	21	AAW23563
43	28	87.5	3443	20	AAW84559
44	27	84.4	37	20	AAW12012
45	27	84.4	225	21	AAW51900

ALIGNMENTS

RESULT 1	
AAW3667	standard; Protein; 331 AA.
AC	AAW3667;
DT	18-OCT-2000 (first entry)
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 44968.
KW	Protein identification; signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter;
KW	termination sequence.
XX	
OS	Arabidopsis thaliana.
PN	EP1033405-A2.
XX	
PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 2000EP-0301439.
XX	
PR	25-FEB-1999; 99US-0121825.
PR	05-MAR-1999; 99US-0123180.
PR	09-MAR-1999; 99US-0123548.
PR	23-MAR-1999; 99US-0125788.
PR	25-MAR-1999; 99US-0126264.
PR	29-MAR-1999; 99US-0126785.
PR	01-APR-1999; 99US-0127462.
PR	06-APR-1999; 99US-0128234.
PR	08-APR-1999; 99US-0128714.
PR	16-APR-1999; 99US-0129845.
PR	19-APR-1999; 99US-0130077.
PR	21-APR-1999; 99US-0130449.

C. purpureus delta
C. purpureus delta
Protein b5pp with
P. patens delta6-d
STN1 (suppressor o
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Subcloned JAK2 pro
JAK2. Mus muscu
Murine JAK2 kinase
Amio acid sequen
JAK2 protein sequ
Human JAK2 kinase
Human JAK2 kinase
Human JAK2 protein
New polypeptide ba
Zee mays protein f
Brucella 17 kDa an
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Arabidopsis thalia
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Arabidopsis thalia
Arabidopsis thalia
Human peripheral n
NanG polypeptide.
Human sodium chann
Polyprotien encode
Human 5' EST secre
Gene 21 human secr

PR 23-APR-1999; 990S-0130510.
PR 23-APR-1999; 990S-0130891.
PR 28-APR-1999; 990S-0131449.
PR 30-APR-1999; 990S-0132048.
PR 30-APR-1999; 990S-0132407.
PR 04-MAY-1999; 990S-0132484.
PR 05-MAY-1999; 990S-0132485.
PR 06-MAY-1999; 990S-0132486.
PR 07-MAY-1999; 990S-0132487.
PR 11-MAY-1999; 990S-0134256.
PR 14-MAY-1999; 990S-0134218.
PR 14-MAY-1999; 990S-0134219.
PR 14-MAY-1999; 990S-0134221.
PR 14-MAY-1999; 990S-0134370.
PR 18-MAY-1999; 990S-0134768.
PR 19-MAY-1999; 990S-0134941.
PR 20-MAY-1999; 990S-0135124.
PR 21-MAY-1999; 990S-0135353.
PR 24-MAY-1999; 990S-0135629.
PR 25-MAY-1999; 990S-0136021.
PR 27-MAY-1999; 990S-0136392.
PR 28-MAY-1999; 990S-0136782.
PR 01-JUN-1999; 990S-0137222.
PR 03-JUN-1999; 990S-0137528.
PR 04-JUN-1999; 990S-0137502.
PR 07-JUN-1999; 990S-0137724.
PR 08-JUN-1999; 990S-0138094.
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PR 14-JUN-1999; 990S-0139119.
PR 16-JUN-1999; 990S-0139452.
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PR 29-OCT-1999; 99US-0162142.

Query Match 100.0%; Score 32; DB 21; Length 331;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDELH 5
Db 117 hdelh 121

RESULT 2

AC AAG36666
ID AAG36666 standard; Protein; 351 AA.

XX AAG36666;

DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 44967.

KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.

PN EP103405-A2.

XX 06-SEP-2000.

PD 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

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PR 25-MAR-1999; 99US-0126264.

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Query Match 100.0%; Score 32; DB 21; Length 351;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDPH 5
 Db 137 hdpH 141

RESULT 3
 AAW84139 standard; Peptide; 355 AA.
 XX AAW84139;
 AC AAW84139;
 DT 15-FEB-1999 (first entry)
 XX
 DE Desaturase enzyme peptide sequence.
 XX
 KW Fatty acid; desaturase; polyunsaturated fatty acid;
 KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
 KW cholesterol level; endometriosis; premenstrual syndrome;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
 XX
 OS Undefined.
 XX
 PN W09846763-A1.
 XX
 PD 22-OCT-1998.
 XX
 PF 10-APR-1998; 98WO-US07126.
 XX
 PR 11-APR-1997; 97US-0834655.
 XX
 PA (ABBO) ABBOTT LAB.
 PA (CALJ) CALGENE LLC.
 PI
 PI Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P;
 PI Thurmond J;
 XX
 DR WPI. 1998-594582/50.
 XX
 PT New isolated fatty acid desaturase enzymes - used for the production
 PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical
 PT compositions, nutritional compositions, cosmetics or animal feed
 XX
 PS Example 2; Pages 101-102; 165pp; English.
 XX
 CC The present sequence represents a peptide derived from a desaturase
 CC enzyme. The specification describes methods for desaturating a
 CC fatty acid and for producing a desaturated fatty acid by expressing
 CC increased levels of a desaturase. Desaturases can be used to produce
 CC desaturating fatty acids. The enzymes can be used to produce
 CC polyunsaturated fatty acids, which can be used for treating malnutrition,
 CC in pharmaceutical compositions, in cosmetics or in animal feed. The

CC polyunsaturated fatty acids can be used for treating e.g. restenosis
CC after angioplasty, inflammation, rheumatoid arthritis, asthma, psoriasis,
CC cancer, diabetes or eczema or reduce blood pressure. They can also be
CC used to inhibit platelet aggregation, cause vasodilation, lower
CC cholesterol levels, inhibit proliferation of vessel wall, smooth muscle
CC and fibrous tissue, reduce or prevent gastro-intestinal bleeding and
CC other side effects caused by non-steroidal anti-inflammatory drugs,
CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic
CC encephalomyelitis and chronic fatigue after viral infections, treat AIDS,
CC multiple sclerosis, acute respiratory syndrome, hypertension and
CC inflammatory skin disorders.

SQ Sequence 355 AA:

Query Match 100.0%; Score 32; DB 19; Length 355;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDFLH 5
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Db 70 hdtfh 74

RESULT 4

AAC36665 AAC36665 standard; Protein; 373 AA.

XX AAC36665;

XX 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 44966.

XX Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana.

XX EPI033405-A2.

XX 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

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PR 06-APR-1999; 99US-0128234.

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PR 04-MAY-1999; 99US-0132407.

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PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.

Query Match	100.0%;	Score 32;	DB 21;	Length 373;
Best Local Similarity	100.0%;	Pred. No. 43;		
Matches 5;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	1 HDEFLH 5 			
Db	159 hdfllh 163			
RESULT 5				
AAM84137				
ID	AAM84137 standard; Protein: 457 AA.			
XX				
AC	AAM84137;			
XX				
DT	15-FEB-1999 (first entry)			
XX				
DE	A delta-6 desaturase enzyme.			
XX				
KM	Fatty acid: delta-6 desaturase; polyunsaturated fatty acid;			
KM	malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;			
KM	cancer; diabetes; eczema; platelet aggregation; vasodilation;			
KM	cholesterol level; endometriosis; premenstrual syndrome;			
KM	myalgia encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;			
KM	acute respiratory syndrome; hypertension; inflammatory skin disorder.			
XX				
OS	Mortierella alpina.			
XX				
PN	W09846763-A1.			
XX				
PD	22-OCT-1998.			
XX				
PF	10-APR-1998; 98WO-US07126.			
XX				
PR	11-APR-1997; 97US-0834655.			
XX				
PA	(ABBO) ABBOTT LAB.			
PA	(CALJ) CALGENE LLC.			
XX				
PI	Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P;			
PI	Thumond J;			
XX				
DR	WPI: 1998-594582/50.			
DR	N-PSDB: AAV63624.			
XX				
PT	New isolated fatty acid desaturase enzymes - used for the production			
PT	of polyunsaturated fatty acids for use in, e.g. pharmaceutical			
PT	compositions, nutritional compositions, cosmetics or animal feed			
XX				
PS	Claim 3; Fig 3A-E; 165pp; English.			
XX				
CC	The present sequence represents a Mortierella alpina fatty acid delta-6			
CC	desaturase enzyme. The enzyme sequence is used in the methods of			
CC	the invention. The specification describes methods for desaturating a			
CC	fatty acid and for producing a desaturated fatty acid by expressing a			
CC	increased levels of a desaturase. The present desaturase is an enzyme			
CC	which introduces a double bond carbons 6 and 7 from the carboxyl end of			
CC	a fatty acid molecule. The enzyme can be used for desaturating fatty			
CC	acids. The enzyme can be used to produce polyunsaturated fatty acids,			
CC	which can be used for treating malnutrition, in pharmaceutical			
CC	compositions, in cosmetics or in animal feed. The polyunsaturated fatty			
CC	acids can be used for treating e.g. restenosis after angioplasty,			
CC	inflammation, rheumatoid arthritis, asthma, psoriasis, cancer, diabetes			
CC	or eczema or reduce blood pressure. They can also be used to inhibit			
CC	platelet aggregation, cause vasodilation, lower cholesterol levels,			
CC				

CC inhibit proliferation of vessel wall smooth muscle and fibrous tissue,
CC reduce or prevent gastro-intestinal bleeding and other side effects
CC caused by non-steroidal anti-inflammatory drugs, prevent or treat
CC endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis
CC and chronic fatigue after viral infections, treat AIDS, multiple
CC sclerosis, acute respiratory syndrome, hypertension and inflammatory skin
CC disorders.
XX
SQ Sequence 457 AA:

Query Match 100.0%; Score 32; DB 19; Length 457;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDELH 5
DB 172 hdelh 176

RESULT 6
AAW95504
ID AAW95504 standard; peptide; 457 AA.
XX
XX AAW95504;
XX
DT 26-MAR-1999 (first entry)
XX
DE Mortierella alpina delta 6 desaturase.
XX
XX Delta 6 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil;
KM polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;
KM stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula;
KM dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;
KM rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;
KM diabetes; cosmetic; animal feed.
XX
XX Mortierella alpina.
XX
XX OS
XX PN MO9846764-A1.
XX PD 22-OCT-1998.
XX PF 10-APR-1998; 98WO-US07421.
XX
XX PR 24-OCT-1997; 97US-0956985.
XX PR 11-APR-1997; 97US-0833610.
XX PR 11-APR-1997; 97US-0834033.
XX PR 11-APR-1997; 97US-0834655.
XX
XX PA (ABBO) ABBOTT LAB.
XX PA (CALJ) CALGENE LLC.
XX
XX PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P;
XX PI Thurmond J;
XX
XX DR MPI: 1999-080739/07.
XX DR N-PSDB; AAX00889.
XX
XX PT Nucleic acid construct able to express fatty acid desaturase in
XX PT plants - useful in human or animal nutrition, as cosmetics and
XX PT therapeutically, e.g. for restenosis, cancer and diabetes
XX
PS Claim 7; Fig 3A-E; 210pp; English.
XX
XX This represents a Mortierella alpina delta 6 desaturase. The invention
XX relates to a nucleic acid construct that contains at least one of the
XX nucleotide sequences (AAX00889 to AAX00891) encoding M. alpina delta 6,
XX delta 12 and delta 5 desaturases (AAW95504 to AAW95506) respectively,
XX coupled to an expression control sequence functional in plants.
XX Recombinant plant cells containing at least one DNA encoding a M. alpina
XX fatty acid desaturase (FAD), can be used for the production of
XX polyunsaturated fatty acid (PUFA). These recombinant cells or plants

CC containing them are used to produce oils such as linoleic acid,
CC arachidonic acid, gamma-linolenic acid, dihomo-gamma-linolenic acid,
CC stearidonic acid and eicosapentaenoic acid (EPA). These plant oils are
CC used: (i) to treat malnutrition; (ii) in infant feeding formulas, or
CC dietary supplements or substitutes, for use in humans or animals; (iii)
CC for treating disorders associated with inadequate consumption or
CC production of PUFA (or their metabolites such as prostaglandins), e.g.
CC restenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis,
CC psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics, and
CC (v) as animal feeds. Fragments of the DNA are used as probes to isolate
CC related coding sequences. Recombinant plants can produce high yields of
CC PUFA, since new pathways can be created and unwanted ones suppressed.
CC Plants can be engineered to express oils of particular PUFA composition,
CC e.g. one similar to that in human milk, and product recovery is simpler
CC than with e.g. fish.
XX
SQ Sequence 457 AA:

Query Match 100.0%; Score 32; DB 20; Length 457;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDELH 5
DB 172 hdelh 176

RESULT 7
AAW85121
ID AAW85121 standard; Protein; 457 AA.
XX
XX AAW85121;
XX
DT 11-FEB-1999 (first entry)
XX
XX A delta-6 desaturase enzyme amino acid sequence.
XX
XX DE
XX KM Fatty acid: delta-6 desaturase; polyunsaturated fatty acid;
XX KM malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
XX KM cancer; diabetes; eczema; platelet aggregation; vasodilation;
XX KM cholesterol level; endometriosis; premenstrual syndrome;
XX KM myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
XX KM acute respiratory syndrome; hypertension; inflammatory skin disorder.
XX
XX OS
XX PN MO9846765-A1.
XX PD 22-OCT-1998.
XX PF 10-APR-1998; 98WO-US07422.
XX
XX PR 11-APR-1997; 97US-0833610.
XX
XX PA (ABBO) ABBOTT LAB.
XX PA (CALJ) CALGENE LLC.
XX
XX PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P;
XX PI Thurmond J;
XX
XX DR MPI: 1999-009334/01.
XX
XX PT New nucleic acid encoding deltas and other desaturase enzymes -
XX PT useful in production of oils of increased arachidonic acid content,
XX PT used, e.g. for treating cancer, as foods, animal feeds and cosmetics
XX
XX PS Disclosure: Pages 95-96; 153pp; English.
XX
XX The present sequence represents a fatty acid delta-6 desaturase enzyme.
XX The specification describes methods for desaturating a fatty acid and
XX for producing a desaturated fatty acid by expressing increased levels of
XX a desaturase. The present desaturase is an enzyme which introduces a

CC double bond carbons 6 and 7 from the carboxyl end of a fatty acid
CC molecule. The enzyme can be used for desaturating fatty acids. The
CC enzyme can be used to produce polyunsaturated fatty acids, which can
CC be used for treating malnutrition. In pharmaceutical compositions,
CC in cosmetics or in animal feed. The polyunsaturated fatty acids can
CC be used for treating e.g. xeroderma after angioplasty, inflammation,
CC rheumatoid arthritis, asthma, psoriasis, cancer, diabetes or eczema
CC or reduce blood pressure. They can also be used to inhibit platelet
CC aggregation, cause vasodilation, lower cholesterol levels, inhibit
CC proliferation of vessel wall smooth muscle and fibrous tissue,
CC reduce or prevent gastro-intestinal bleeding and other side effects
CC caused by non-steroidal anti-inflammatory drugs, prevent or treat
CC endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis
CC and chronic fatigue after viral infections, treat AIDS, multiple
CC sclerosis, acute respiratory syndrome, hypertension and inflammatory skin
CC disorders.

XX Sequence 457 AA:

Query Match 100.0%; Score 32; DB 20; Length 457;

Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDEFLH 5

DB 172 hdfllh 176

RESULT 8

AAV92599 AAV92599 standard; Protein: 457 AA.

XX AAV92599;

DT 10-AUG-2000 (first entry)

XX M. alpina delta-6 fatty acid desaturase.

XX delta-6-desaturase; gamma-linolenic acid; biosynthesis;
KW transgenic insect cell; polyunsaturated long chain fatty acid;
KW antiinflammatory; antirheumatic; antidiabetic; antiparasitic;
KW osteopathic; cytostatic; antidiabetic; dermatological; gynecological;
KW anti-HIV; neuroprotective; hypotensive; nephroprotective; vasodilator;
KW antiaggregant; vasotropic.

XX Mortierella alpina.

XX Key Location/Qualifiers

FT MISC-difference 172..176

FT MISC-difference 209..213

FT MISC-difference 395..399

FT MISC-difference 395..399

FT MISC-difference 395..399

XX WO200020602-A2.

XX 13-APR-2000.

XX 29-SEP-1999; 99WO-US22686.

XX 05-OCT-1998; 98US-0103110.

XX (ABBO) ABBOTT LAB.

XX Mukerji P, Huang Y, Parker-Barnes JM, Das T;

XX WPI; 2000-328935/28.

XX N-PSDB; AAA09430.

XX Novel transgenic insect cells comprising a nucleotide sequence which
PT encode delta-6-desaturase or delta-12-desaturase, useful for producing
PT poly-unsaturated long chain fatty acids, e.g. arachidonic acid

PS Claim 1; Page 145-146; 170pp; English.

XX The fatty acid desaturases are able to catalyse the conversion of oleic
CC alpha-linolenic acid, linoleic acid to gamma-linolenic acid or of
CC alpha-linolenic acid to stearidonic acid. Transgenic insect cells
CC comprising a nucleotide sequence which encodes a polypeptide comprising
CC residues 50-53, 39-43, 172-176, 204-213, or 390-402 of delta-6
CC desaturase (AAV92599) or comprising delta-12 desaturase (AAV92600) are
CC claimed. Oil and fatty acids (especially gamma-linolenic acid) isolated
CC from the recombinant insect cells are also claimed. Production of
CC polyunsaturated long chain fatty acids (PUFAs) in insect cells has many
CC advantages, as insect cells have greatly simplified lipid compositions,
CC are not subject to external variable fluctuations, and can easily be
CC maintained and manipulated. The oils are used in pharmaceutical
CC compositions, infant formulas, dietary supplements or substitutes, and
CC cosmetics (all claimed). The PUFAs supplements have antiinflammatory,
CC antirheumatic, antidiabetic, antiparasitic, osteopathic, cytostatic,
CC antidiabetic, dermatological, gynecological, anti-HIV, neuroprotective,
CC hypotensive, nephroprotective, vasodilator, antiaggregant and vasotropic
CC activity.

XX Sequence 457 AA:

Query Match 100.0%; Score 32; DB 21; Length 457;

Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDEFLH 5

DB 172 hdfllh 176

RESULT 9

AAV56045 AAV56045 standard; Protein: 457 AA.

XX AAV56045;

DT 28-MAR-2000 (first entry)

XX Fungal delta6-desaturase protein sequence.

XX Polyunsaturated fatty acid; fungus; delta6-desaturase; animal feed;

XX transgenic animal; malnutrition; biosynthesis.

XX Unidentified.

XX WO9961602-A1.

XX 02-DEC-1999.

XX 28-MAY-1999; 99WO-US12088.

XX 29-MAY-1998; 98US-0087578.

XX (OHS) UNIV OHIO STATE.

XX Kopechick JJ, Kelder B, Huang Y, Kirchner SJ, Mukerji P;

XX WPI; 2000-072619/06.

XX N-PSDB; AAZ47129.

XX Producing essential fatty acids and long-chain polyunsaturated fatty

XX acids, for use in nutritional, animal feed and medical formulations -

XX Disclosure; Fig 9; 71pp; English.

CC The invention relates to a method of generating novel compositions
CC comprising animal cells producing essential fatty acids (FAs). The animal
CC cells are produced by transforming cells, e.g. embryonic stem cells, with
CC nucleic acid encoding heterologous enzymes involved in fatty acid,
CC e.g. long chain or polyunsaturated fatty acid (PFA) biosynthesis. This
CC sequence corresponds to a fungal delta6-desaturase whose coding sequence
CC is an example of a nucleic acid sequence used to transform the cells. The
CC essential FAs obtained can be used in nutritional formulations or animal
CC feed formulations. The long chain PFAs can be used in nutritional
CC formulations, cosmetic formulations or animal feed formulations. The
CC products can also be used for producing transgenic animals which can be
CC used for producing essential FAs which can be used for producing
CC downstream products such as leukotrienes, thromboxanes, arachidonic acid,
CC eicosapentaenoic acid or docosahexaenoic acid. The products can also be
CC used in cell culture. The animal or milk fat produced can be administered
CC to treat malnutrition.

CC Sequence 457 AA:

Query Match 100.0%; Score 32; DB 21; Length 457;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDEFLH 5
| | | | |
DB 172 hdfllh 176

RESULT 10

AAB31684
ID AAB31684 standard; Protein: 457 AA.

AC AAB31684;

DT 30-APR-2001 (first entry)

DE Amino acid sequence of a fungal delta6 desaturase.

KW delta6 desaturase; desaturase gene; elongase gene; fatty acid;

KW dietary substitute; animal feed.

OS Mortierella alpina.

PN WO200104636-A1.

PD 18-JAN-2001.

PF 11-JUL-2000; 2000WO-US19011.

PR 12-JUL-1999; 99US-0351525.

PA (UYOH-) UNIV OHIO.

PI Kopchick JT, Kelder B;

DR MPI: 2001-182622/18.

N-PSDB; AAF25234.

CC New compositions comprising cells that express desaturases and
CC elongases, for synthesizing essential fatty acids or long-chain
CC polyunsaturated fatty acids, used in nutritional, cosmetic or animal
CC feed formulations

PS Disclosure; Fig 9; 93pp; English.

CC The present sequence represents a delta6 desaturase. The desaturase
CC polynucleotide sequence was used to transfect mammalian cells, to
CC produce animal cells expressing a desaturase gene and/or an elongase
CC gene. Compositions comprising cells of the invention are useful for
CC synthesizing essential fatty acids, their derivatives or downstream
CC products, as well as altered levels of long-chain polyunsaturated

CC fatty acids and eicosanoids. The compositions are useful in nutritional
CC formulae, e.g. infant formula, dietary supplements or dietary
CC substitutes for both humans and animals. The compositions are also
CC useful in cosmetic or animal feed formulations. Furthermore, the
CC compositions may also be used as fat free media or as research reagents.

CC Sequence 457 AA:

Query Match 100.0%; Score 32; DB 22; Length 457;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDEFLH 5
| | | | |
DB 172 hdfllh 176

RESULT 11

AAB46435
ID AAB46435 standard; Protein: 483 AA.

AC AAB46435;

DT 06-APR-2001 (first entry)

DE C. purpureus delta6-acetylase/delta6-desaturase SFQ ID NO 2.

KW Delta6-acetylase; delta6-desaturase; unsaturated fatty acid;

KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;

KW cosmetic.

OS Ceratodon purpureus.

PN WO200075341-A1.

PD 14-DEC-2000.

PF 07-JUN-2000; 2000WO-EP05274.

PR 07-JUN-1999; 99DE-1025718.

PR 22-DEC-1999; 99DE-1062409.

PA (BADL) BASF AG.

PI Heinz E, Stryme S, Lee M, Girke T, Sperling P, Zaeheringer U;

DR MPI: 2001-112150/12.

N-PSDB; AAF25729.

PT Nucleic acid encoding delta6-acetylase or desaturase, useful for
PT producing plant oils with increased content of unsaturated fatty acids

PS Example 8; Page 44-46; 69pp; German.

CC This invention describes a novel isolated nucleic acid (I) encoding
CC polypeptides (II) with Delta6-acetylase and/or Delta6-desaturase
CC activity. The invention also describes (a) amino acid sequences encoded
CC by (I); (b) an expression cassette (EC) containing (I) linked to one or
CC more regulatory sequences; (c) a vector containing (I) and EC; (d)
CC organisms containing (I), EC or the vectors of (c); (e) preparation of
CC unsaturated fatty acids (A) or triglycerides (TG) with increased content
CC of (A) by introducing (I) or EC into an oil-producing organism; (f)
CC proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)
CC production of (A) or TG by using (Ia); and (h) (A) and TG produced by
CC method (g). (I) are used to produce transgenic plants (or other
CC organisms) that produce oils or triglycerides (TG) with increased content
CC of unsaturated fatty acids (A) and to isolate related sequences by
CC homology screening. (A), or TG containing them, are useful in human
CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes,
CC can be used to suppress expression of (II), resulting in oils with

CC Increased content of saturated fatty acids.
XX Sequence 483 AA;
SQ

Query Match 100.0%; Score 32; DB 22; Length 483;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDELH 5
| | | | |
Db 212 hdelh 216

RESULT 12

AAB46436
ID AAB46436 standard; Protein: 483 AA.

XX AAB46436;

DT 06-APR-2001 (first entry)

DE C. purpureus delta6-acetylase/delta6-desaturase SEQ ID NO 4.

XX Delta6-acetylase; delta6-desaturase; unsaturated fatty acid;
KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;
KW cosmetic.

XX Ceratodon purpureus.

XX WO200075341-A1.

XX 14-DEC-2000.

XX 07-JUN-2000; 2000WO-EP05274.

XX 07-JUN-1999; 99DE-1025718.

XX 22-DEC-1999; 99DE-1062409.

XX (BADI) BASF AG.

PI Heinz E, Stymer S, Lee M, Girke T, Sperling P, Zaehring U;

DR WPI; 2001-112150/12.

DR N-PSDB; AAF25730.

PT Nucleic acid encoding delta6-acetylase or desaturase, useful for
producing plant oils with increased content of unsaturated fatty acids

PS Example 8; Page 49-50; 69pp; German.

XX This invention describes a novel isolated nucleic acid (I) encoding
polypeptides (II) with Delta6-acetylase and/or Delta6-desaturase
activity. The invention also describes (a) amino acid sequences encoded
by (I); (b) an expression cassette (EC) containing (I) linked to one or
more regulatory sequences; (c) a vector containing (I) and EC; (d)
organisms containing (I), EC or the vectors of (c); (e) preparation of
unsaturated fatty acids (A) or triglycerides (TG) with increased content
of (A) by introducing (I) or EC into an oil-producing organism; (f)
production of (A) or TG by using (Ia); and (h) (A) and TG produced by
method (g). (I) are used to produce transgenic plants (or other
organisms) that produce oils or triglycerides (TG) with increased content
of unsaturated fatty acids (A) and to isolate related sequences by
homology screening. (A), or TG containing them, are useful in human
nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes,
can be used to suppress expression of (II), resulting in oils with
increased content of saturated fatty acids.

XX Sequence 483 AA;

SQ

Query Match 100.0%; Score 32; DB 22; Length 483;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDELH 5
| | | | |
Db 212 hdelh 216

RESULT 13

AAB46440
ID AAB46440 standard; Protein: 520 AA.

XX AAB46440;

DT 06-APR-2001 (first entry)

DE C. purpureus delta6-acetylase/delta6-desaturase SEQ ID NO 12.

XX Delta6-acetylase; delta6-desaturase; unsaturated fatty acid;
KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;
KW cosmetic.

XX Ceratodon purpureus.

XX WO200075341-A1.

XX 14-DEC-2000.

XX 07-JUN-2000; 2000WO-EP05274.

XX 07-JUN-1999; 99DE-1025718.

XX 22-DEC-1999; 99DE-1062409.

XX (BADI) BASF AG.

PI Heinz E, Stymer S, Lee M, Girke T, Sperling P, Zaehring U;

DR WPI; 2001-112150/12.

DR N-PSDB; AAF25734.

PT Nucleic acid encoding delta6-acetylase or desaturase, useful for
producing plant oils with increased content of unsaturated fatty acids

PS Example 7; Page 57-59; 69pp; German.

XX This invention describes a novel isolated nucleic acid (I) encoding
polypeptides (II) with Delta6-acetylase and/or Delta6-desaturase
activity. The invention also describes (a) amino acid sequences encoded
by (I); (b) an expression cassette (EC) containing (I) linked to one or
more regulatory sequences; (c) a vector containing (I) and EC; (d)
organisms containing (I), EC or the vectors of (c); (e) preparation of
unsaturated fatty acids (A) or triglycerides (TG) with increased content
of (A) by introducing (I) or EC into an oil-producing organism; (f)
production of (A) or TG by using (Ia); and (h) (A) and TG produced by
method (g). (I) are used to produce transgenic plants (or other
organisms) that produce oils or triglycerides (TG) with increased content
of unsaturated fatty acids (A) and to isolate related sequences by
homology screening. (A), or TG containing them, are useful in human
nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes,
can be used to suppress expression of (II), resulting in oils with
increased content of saturated fatty acids.

XX Sequence 520 AA;

SQ

Query Match 100.0%; Score 32; DB 22; Length 520;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDFLH 5
 DB 249 hdfllh 253

RESULT 14

AA51354
 ID AAY51354 standard; Protein; 525 AA.

AC AAY51354;

DT 27-APR-2000 (first entry)

DE Protein b5pp with delta6 fatty acid desaturase activity.

XX Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid;
 KM transgenic plant; crop plant; delta-8-unsaturated long-chain base;
 KM tolerance; resistance; soil salinity; ion stress; toxicity; drought;
 KM cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
 KM pharmaceutical; food; chemical raw material.

OS Unidentified.

PN DE19828850-A1.

PD 30-DEC-1999.

PF 27-JUN-1998; 98DE-1028850.

PR 27-JUN-1998; 98DE-1028850.

XX (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.

PI Heinz E, Zaehlinger U, Schmidt H, Sperling P;

DR WPI; 2000-127549/12.

XX New sphingolipid desaturase that selectively introduces double bond

PT into sphingolipids and capnoids -

PS Disclosure; Fig 16; 62pp; German.

XX This invention describes a novel sphingolipid desaturase that selectively
 CC introduces a double bond into the sphingobase of the ceramide residue of
 CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
 CC desaturase, or a vector containing the DNA sequence, can be used to
 CC produce transgenic plants, especially crop plants, with an increased or
 CC decreased delta-8-unsaturated long-chain base content or an altered
 CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
 CC compensate for a delta-8-unsaturated long-chain base deficiency, to
 CC exclude production of delta-8-unsaturated bases, to increase tolerance
 CC or resistance to soil salinity, ion stress or toxicity, drought, wet
 CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
 CC alter size growth and flowering time. Cells, transgenic organisms or
 CC plants containing the DNA sequence can be used to produce sphingolipids
 CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
 CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
 CC materials. This sequence represents a protein which has delta6 fatty acid
 CC desaturase activity which is described in the method of the invention.

XX Sequence 525 AA;

Query Match 100.0%; Score 32; DB 21; Length 525;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDFLH 5
 DB 254 hdfllh 258

RESULT 15

AA46810
 ID AAB46810 standard; Protein; 525 AA.

AC AAB46810;

DT 23-APR-2001 (first entry)

DE P. patens delta6-desaturase protein.

XX Delta6-desaturase; unsaturated fatty acid; transgenic; oil; lipid;
 KM fatty acid; human nutrition; animal nutrition; cosmetic; pharmaceutical;
 KM agricultural chemical.

OS Physcomitrella patens.

PN WO200102591-A1.

PD 11-JAN-2001.

PF 04-JUL-2000; 2000WO-EP06223.

PR 06-JUL-1999; 98US-0347531.

PR 30-JUN-2000; 2000DE-1030976.

PA (BADI) BASF AG.

PI Heinz E, Girke T, Scheffler J, Da Costa Silva EO;

DR WPI; 2001-123117/13.

DR N-PSDB; AAF26040.

PT Production of unsaturated fatty acids; useful e.g. in nutrition,
 PT cosmetics or pharmaceuticals; in organisms transformed with
 PT Physcomitrella patens delta-6-desaturase nucleic acid -

PS Claim 1c; Page 41-43; 49pp; German.

XX This invention describes a novel preparation of unsaturated fatty acids
 CC (I) by introducing into an organism at least one isolated nucleic acid
 CC (II) that encodes a polypeptide (III) with Delta6-desaturase activity.
 CC Organisms that contain at least 1 wt.% (I), on total fatty acid content,
 CC are then selected. (II) is selected from: (a) a 2012 bp sequence (S1),
 CC defined in the specification, or its equivalents within the degeneracy of
 CC the genetic code; or (b) derivatives of the sequence of (a) that encode a
 CC 525 amino acid polypeptide (S2), defined in the specification, or a
 CC polypeptide with at least 50% homology with (S2) and practically the same
 CC enzymatic activity. The invention also describes (1) transgenic organisms
 CC that contain (II); and (2) oils, lipids and fatty acids produced by the
 CC new method. The oils, lipids and fatty acids produced by the transformed
 CC organisms are used in human or animal nutrition, cosmetics,
 CC pharmaceuticals and agricultural chemicals. (III) can also be used, in
 CC vitro, for increasing the (I) content of triglycerides. The transgenic
 CC organisms have increased contents of (I), or of (I)-containing
 CC triglycerides, particularly of gamma-linolenic acid.

XX Sequence 525 AA;

Query Match 100.0%; Score 32; DB 22; Length 525;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDFLH 5
 DB 254 hdfllh 258

Search completed: August 9, 2001, 20:24:15
 Job time: 249 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 9, 2001, 20:25:06 ; Search time 45.84 Seconds
(without alignments)
2.246 Million cell updates/sec

Title: US-09-367-013b-2_COPY_172_176
Perfect score: 32
Sequence: 1 HDTLH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
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4: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfil1sl.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	100.0	355	2 US-08-834-655-5	Sequence 5, Appl1
2	32	100.0	355	3 US-08-834-033A-6	Sequence 6, Appl1
3	32	100.0	355	4 US-09-363-574-5	Sequence 5, Appl1
4	32	100.0	457	2 US-08-834-655-2	Sequence 2, Appl1
5	32	100.0	457	2 US-08-834-610-4	Sequence 4, Appl1
6	32	100.0	457	3 US-08-834-033A-2	Sequence 2, Appl1
7	32	100.0	457	3 US-08-834-033A-14	Sequence 14, Appl1
8	32	100.0	457	4 US-09-363-574-2	Sequence 2, Appl1
9	32	100.0	582	1 US-08-431-080-16	Sequence 16, Appl1
10	32	100.0	582	1 US-08-938-534-16	Sequence 16, Appl1
11	29	90.6	294	4 US-09-046-158A-5	Sequence 5, Appl1
12	29	90.6	971	1 US-08-446-038B-19	Sequence 19, Appl1
13	29	90.6	971	1 US-08-446-010B-19	Sequence 19, Appl1
14	29	90.6	971	1 US-08-805-445-19	Sequence 19, Appl1
15	29	90.6	971	2 US-08-064-067D-19	Sequence 19, Appl1
16	29	90.6	971	2 US-09-066-208-19	Sequence 19, Appl1
17	29	90.6	993	1 US-08-446-010B-25	Sequence 25, Appl1
18	29	90.6	1129	1 US-08-357-598-6	Sequence 6, Appl1
19	29	90.6	1129	1 US-08-097-997A-9	Sequence 9, Appl1
20	29	90.6	1129	2 US-08-567-508C-3	Sequence 3, Appl1
21	29	90.6	1129	2 US-09-003-289-6	Sequence 6, Appl1
22	29	90.6	1129	3 US-09-196-480-3	Sequence 3, Appl1
23	29	90.6	1129	4 US-08-665-574C-9	Sequence 9, Appl1
24	29	90.6	1129	4 US-08-946-994-9	Sequence 9, Appl1
25	29	90.6	1129	5 PCT-US95-16435-6	Sequence 6, Appl1
26	29	90.6	1132	2 US-08-367-508C-2	Sequence 2, Appl1
27	29	90.6	1132	3 US-09-196-480-2	Sequence 2, Appl1

28	29	90.6	1139	4 US-09-046-158A-22	Sequence 22, Appl1
29	28	87.5	1956	4 US-08-843-417-10	Sequence 10, Appl1
30	28	87.5	3443	2 US-08-416-603-2	Sequence 2, Appl1
31	27	84.4	1184	1 US-08-446-038B-20	Sequence 20, Appl1
32	27	84.4	1184	1 US-08-446-010B-20	Sequence 20, Appl1
33	27	84.4	1184	2 US-08-805-445-20	Sequence 20, Appl1
34	27	84.4	1184	2 US-08-064-067D-20	Sequence 20, Appl1
35	27	84.4	1187	1 US-09-066-208-20	Sequence 20, Appl1
36	27	84.4	1187	1 US-08-357-598-8	Sequence 8, Appl1
37	27	84.4	1187	1 US-08-097-997A-13	Sequence 13, Appl1
38	27	84.4	1187	2 US-09-003-289-8	Sequence 8, Appl1
39	27	84.4	1187	4 US-08-665-574C-13	Sequence 13, Appl1
40	27	84.4	1187	4 US-08-946-994-13	Sequence 13, Appl1
41	27	84.4	1187	5 PCT-US95-16435-8	Sequence 8, Appl1
42	26	81.2	13	1 US-07-890-422B-36	Sequence 36, Appl1
43	26	81.2	44	1 US-07-890-422B-4	Sequence 4, Appl1
44	26	81.2	138	1 US-08-309-512-7	Sequence 7, Appl1
45	26	81.2	138	5 PCT-US92-08756A-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-08-834-655-5
; Sequence 5, Application US/08834655
; Patent No. 5968809
GENERAL INFORMATION:
APPLICANT: KNOTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSES:
ADDRESSEE: RAE-VENTER LAW GROUP, P. C.
STREET: 260 SHERIDAN AVENUE, P. O. BOX 60039
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-Apr-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.124.000S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-655-5

Query Match 100.0%; Score 32; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDELH 5
11111
DB 70 HDELH 74

RESULT 2

US-08-834-033A-6
Sequence 6, Application US/08834033A
Patent No. 6075183

GENERAL INFORMATION:

APPLICANT: KNUZON, DEBORAH
APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.

STREET: 2001 FERRY BUILDING

CITY: SAN FRANCISCO

STATE: CA

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/834,033A

FILING DATE: 11-APR-1997

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: WARD, MICHAEL R.

REGISTRATION NUMBER: 38,651

REFERENCE/DOCKET NUMBER: CGAB-300.USA

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 433-4150

TELEFAX: (415) 433-8716

TELEX: N/A

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 355 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-834-033A-6

Query Match 100.0%; Score 32; DB 3; Length 355;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDELH 5
11111
DB 70 HDELH 74

RESULT 3

US-09-363-574-5
Sequence 5, Application US/09363574
Patent No. 6136574

GENERAL INFORMATION:

APPLICANT: KNUZON, DEBORAH

APPLICANT: MUKERJI, PRADIP

APPLICANT: HUANG, YUNG-SHENG

APPLICANT: THURMOND, JENNIFER

APPLICANT: CHAUDHARY, SUNITA

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:

ADDRESSEE: LIMBACH AND LIMBACH L.L.P.

STREET: 2001 FERRY BUILDING

CITY: SAN FRANCISCO

STATE: CA

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/363,574

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: WARD, MICHAEL R.

REGISTRATION NUMBER: 38,651

REFERENCE/DOCKET NUMBER: CGAB-202 USA

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 433-4150

TELEFAX: (415) 433-8716

TELEX: N/A

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 355 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-363-574-5

Query Match 100.0%; Score 32; DB 4; Length 355;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDELH 5
11111
DB 70 HDELH 74

RESULT 4

US-08-834-655-2
Sequence 2, Application US/08834655
Patent No. 5968809

GENERAL INFORMATION:

APPLICANT: KNUZON, DEBORAH

APPLICANT: MUKERJI, PRADIP

APPLICANT: HUANG, YUNG-SHENG

APPLICANT: THURMOND, JENNIFER

APPLICANT: CHAUDHARY, SUNITA

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: RAE-VENTER LAW GROUP, P.C.

STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039

CITY: PALO ALTO

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/834,655

FILING DATE: 11-APR-1997

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.124.0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-655-2

Query Match 100.0%; Score 32; DB 2; Length 457;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDPFLH 5
DB 172 HDPFLH 176

RESULT 5
US-08-833-610-4

Sequence 4, Application US/08833610
Patent No. 5972664

GENERAL INFORMATION:

APPLICANT: KNUITZON, DEBORAH

APPLICANT: MURKERT, PRADIP

APPLICANT: HUANG, YUNG-SHENG

APPLICANT: THURMOND, JENNIFER

APPLICANT: CHAUDHARY, SUNITA

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: RAE-VENTER LAW GROUP, P.C.

STREET: 260 SHERIDAN AVE, P.O. BOX 60039

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/833,610

FILING DATE: 11-APR-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: RAE-VENTER, BARBARA

REGISTRATION NUMBER: 32,750

REFERENCE/DOCKET NUMBER: CGNE.123.0005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650)328-4400

TELEFAX: (650)328-4477

TELEX: N/A

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 457 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-833-610-4

Query Match 100.0%; Score 32; DB 2; Length 457;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDPFLH 5
DB 172 HDPFLH 176

RESULT 6
US-08-834-033A-2

Sequence 2, Application US/08834033A
Patent No. 6075183

GENERAL INFORMATION:

APPLICANT: KNUITZON, DEBORAH

APPLICANT: MURKERT, PRADIP

APPLICANT: HUANG, YUNG-SHENG

APPLICANT: THURMOND, JENNIFER

APPLICANT: CHAUDHARY, SUNITA

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.

STREET: 2001 FERRY BUILDING

CITY: SAN FRANCISCO

STATE: CA

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/834,033A

FILING DATE: 11-APR-1997

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: WARD, MICHAEL R.

REGISTRATION NUMBER: 38,651

REFERENCE/DOCKET NUMBER: CGAB-300.USA

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 433-4150

TELEFAX: (415) 433-8716

TELEX: N/A

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 457 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-834-033A-2

Query Match 100.0%; Score 32; DB 3; Length 457;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDPFLH 5
DB 172 HDPFLH 176

RESULT 7
US-08-834-033A-14

Sequence 14, Application US/08834033A

Patent No. 6075183

GENERAL INFORMATION:

APPLICANT: KNUITZON, DEBORAH

APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,033A
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300.USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-033A-14

Query Match 100.0%; Score 32; DB 3; Length 457;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDELH 5
|||||
Db 172 HDELH 176

RESULT 8
US-09-363-574-2
Sequence 2, Application US/09363574
Patent No. 6136574
GENERAL INFORMATION:
APPLICANT: KNUZON, DEBORAH
APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,574
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-202 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-363-574-2

Query Match 100.0%; Score 32; DB 4; Length 457;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDELH 5
|||||
Db 172 HDELH 176

RESULT 9
US-08-431-080-16
Sequence 16, Application US/08431080
Patent No. 5698686
GENERAL INFORMATION:
APPLICANT: Gottschling, Daniel E.
APPLICANT: Slinger, William S.
TITLE OF INVENTION: Telomerase Compositions and Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,080
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SN 08/326,781
FILING DATE: October 20, 1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:155/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 582 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-431-080-16

Query Match 100.0%; Score 32; DB 1; Length 582;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDELH 5
|||||
DB 343 HDELH 347

RESULT 10
US-08-938-534-16
Sequence 16, Application US/08938534
Patent No. 5916752
GENERAL INFORMATION:
APPLICANT: Gottschling, Daniel E.
APPLICANT: Slinger, Miriam S.
TITLE OF INVENTION: Telomerase Compositions and Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,534
FILING DATE: 26-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,080
FILING DATE:
APPLICATION NUMBER: SN 08/326,781
FILING DATE: October 20, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:155/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 582 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-938-534-16

Query Match 100.0%; Score 32; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDELH 5
|||||
DB 343 HDELH 347

RESULT 11
US-09-046-158A-5

Sequence 5, Application US/09046158A
Patent No. 6187552
GENERAL INFORMATION:
APPLICANT: Roberts, Steven L.
APPLICANT: Kayles, Paul S.
TITLE OF INVENTION: METHOD FOR IDENTIFYING INHIBITORS OF
TITLE OF INVENTION: JAK2/CYTOKINE RECEPTOR BINDING
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharmacia & Upjohn Co., Intellectual Property
STREET: 301 Henrietta Street
CITY: Kalamazoo
STATE: MI
COUNTRY: USA
ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,158A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Darinley Jr., James D.
REGISTRATION NUMBER: 33,673
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616/833-2210
TELEFAX: 616/833-8897
TELEX: 224401
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-046-158A-5

Query Match 90.6%; Score 29; DB 4; Length 294;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDELH 5
|||||
DB 159 HDELH 163

RESULT 12
US-08-446-038B-19
Sequence 19, Application US/08446038B
Patent No. 5658791
GENERAL INFORMATION:
APPLICANT: Milks, Andrew F.; Ziemlecki, Andrew;
APPLICANT: Harput, Ailsa
TITLE OF INVENTION: No. 5658791el Protein Tyrosine Kinase
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,038B
FILING DATE: 19-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,067
FILING DATE: 30-Jun-1993
APPLICATION NUMBER: PCT/US91/08889
FILING DATE: 26-No. 5658791-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: Australian PK3594/90
FILING DATE: 28-No. 5658791-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: Australian 88229/91
FILING DATE: 27-No. 5658791-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5658791man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5244
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 971 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-446-038B-19

Query Match 90.6%; Score 29; DB 1; Length 971;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDEFLH 5
|||:|
Db 16 HDEFLH 20

RESULT 13
US-08-446-010B-19
Sequence 19, Application US/08446010B
Patent No. 5716818
GENERAL INFORMATION:
APPLICANT: Wilks, Andrew F.; Ziemlecki, Andrew;
APPLICANT: Harpur, Ailsa
TITLE OF INVENTION: No. 5716818el Protein Tyrosine Kinase
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felife & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,010B
FILING DATE: 19-May-1995
CLASSIFICATION: 433
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,038
FILING DATE: 19-May-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,067
FILING DATE: 30-Jun-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/08889
FILING DATE: 26-No. 5716818-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: Australian PK3594/90
FILING DATE: 28-No. 5716818-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: Australian 88229/91
FILING DATE: 27-No. 5716818-1991
ATTORNEY/AGENT INFORMATION:
NAME: Baer, Madeline F.
REGISTRATION NUMBER: 36,437
REFERENCE/DOCKET NUMBER: LUD 5244.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 971 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-446-010B-19

Query Match 90.6%; Score 29; DB 1; Length 971;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDEFLH 5
|||:|
Db 16 HDEFLH 20

RESULT 14
US-08-805-445-19
Sequence 19, Application US/08805445
Patent No. 5821069
GENERAL INFORMATION:
APPLICANT: Wilks, Andrew F.; Ziemlecki, Andrew;
APPLICANT: Harpur, Ailsa
TITLE OF INVENTION: No. 5821069el Protein Tyrosine Kinase
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felife & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,445
FILING DATE: 25-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,038
FILING DATE: 19-MAY-1995
APPLICATION NUMBER: 08/064,067
FILING DATE: 30-Jun-1993
APPLICATION NUMBER: PCT/US91/08889
FILING DATE: 26-No. 5821069-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: Australian PK3594/90
FILING DATE: 28-No. 5821069-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: Australian 88229/91
FILING DATE: 27-No. 5821069-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5821069man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5244
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200

TELEFAX: 212-838-3884
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 971 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-805-445-19

Search completed: August 9, 2001, 20:25:07
 Job time: 206 sec

Query Match 90.6%; Score 29; DB 2; Length 971;
 Best Local Similarity 80.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDELH 5
 |||:|
 Db 16 HDEFVH 20

RESULT 15
 US-08-064-067D-19
 Sequence 19, Application US/08064067D
 Patent No. 5852184
 GENERAL INFORMATION:
 APPLICANT: Wilks, Andrew F.; Ziemiecki, Andrew;
 APPLICANT: Harpur, Alisa
 TITLE OF INVENTION: No. 5852184el Protein Tyrosine Kinase
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Felle & Lynch
 STREET: 805 Third Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: diskette, 3.5 inch, 360 kb storage
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/064,067D
 FILING DATE: 30-Jun-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US91/08889
 FILING DATE: 26-No. 5852184-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: Australian PK3594/90
 FILING DATE: 28-No. 5852184-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: Australian 88229/91
 FILING DATE: 27-No. 5852184-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. 5852184man D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LUD 5244
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-688-9200
 TELEFAX: 212-838-3884
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 971 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-064-067D-19

Query Match 90.6%; Score 29; DB 2; Length 971;
 Best Local Similarity 80.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDELH 5
 |||:|
 Db 16 HDEFVH 20

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OM protein - protein search, using sw model

Run on: August 9, 2001, 20:36:49 ; Search time 28.86 Seconds
(without alignments)
5.935 Million cell updates/sec

Title: US-09-367-013b-2_COPY_172_176
Perfect score: 32
Sequence: 1 HDPLH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	93.8	371	Y028_ARCFU	030207 archaeoglob
2	29	90.6	307	MYIM_SALTY	P37168 salmonella
3	29	90.6	1129	JAK2_MOUSE	062120 mus musculu
4	29	90.6	1132	JAK2_HUMAN	060674 homo sapien
5	29	90.6	1132	JAK2_RAT	062689 rattus norv
6	28	87.5	104	YGEI_YEAST	P53182 saccharomyc
7	28	87.5	158	RISB_BRUAB	Q44688 bruceella ab
8	28	87.5	163	YE99_MYCOP	P75288 mycoplasma
9	28	87.5	209	Y038_NEVOP	005125 oryza pseu
10	28	87.5	263	BZTD_RHOCA	052666 rhodobacter
11	28	87.5	551	TREC_ECOLI	P28904 escherichia
12	28	87.5	561	TREC_BACSU	P39795 bacillus su
13	28	87.5	700	MEPB_HUMAN	Q16820 homo sapien
14	28	87.5	704	MEPB_MOUSE	061847 mus musculu
15	28	87.5	704	MEPB_RAT	P28826 rattus norv
16	28	87.5	1682	CIN6_HUMAN	001118 homo sapien
17	28	87.5	1836	CIN4_HUMAN	P35499 homo sapien
18	28	87.5	2005	CIN2_HUMAN	Q99250 homo sapien
19	27	84.4	78	IBB2_PHAAN	P01061 phaseolus a
20	27	84.4	84	DHSD_CHOCR	P54323 chondrus cr
21	27	84.4	114	CPCL_CANPG	P81580 cancer pagu
22	27	84.4	160	GLBY_CHITP	P18968 chironomus
23	27	84.4	241	CBIH_SALTY	P19732 drosophila
24	27	84.4	263	COO4_SALTY	P91428 salmonella
25	27	84.4	306	COO4_YEAST	P91428 caenorhabdi
26	27	84.4	364	YBBB_ECOTI	O13525 saccharomyc
27	27	84.4	396	O45B_DROME	P33667 escherichia
28	27	84.4	517	DMPN_PSESP	O9V589 pseudomonas
29	27	84.4	518	YX23_CAEEL	O11194 caenorhabdi
30	27	84.4	558	P4HA_CAEEL	O10576 caenorhabdi
31	27	84.4	614	VEI_HPV41	P27351 human papil
32	27	84.4	922	YKFO_YEAST	P35736 saccharomyc
33	27	84.4	1187	TYK2_HUMAN	P29597 homo sapien

34	26	81.2	123	1	PHF5_DESVH	P07603 desulfovibr
35	26	81.2	132	1	F802_SCHMA	P16464 schistosoma
36	26	81.2	146	1	HBH_ALIMI	P02130 alligator m
37	26	81.2	160	1	Y4IN_RHISN	P55554 rhizobium s
38	26	81.2	201	1	ARA5_ARAHY	P04149 arachis hyp
39	26	81.2	248	1	PSPA_HUMAN	P07714 homo sapien
40	26	81.2	251	1	COAT_PYMV	P27255 potato yell
41	26	81.2	284	1	YURL_BACSU	O32153 bacillus su
42	26	81.2	357	1	YHG2_YEAST	P38702 saccharomyc
43	26	81.2	399	1	LGL1_MAIZE	O04003 zea mays (m
44	26	81.2	406	1	TRPB_CAUCR	P12280 caulobacter
45	26	81.2	438	1	XYLA_THEET	P22842 thermosnaer

ALIGNMENTS

RESULT	ID	Y028_ARCFU	STANDARD:	PRT:	371 AA.
AC	030207				
DT	15-JUL-1998 (Rel. 36, Created)				
DT	15-JUL-1998 (Rel. 36, Last sequence update)				
DT	15-JUL-1998 (Rel. 36, Last annotation update)				
DE	HYPOTHETICAL PROTEIN AF0028.				
GN	AF0028.				
OS	Archaeoglobus fulgidus.				
OC	Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;				
OC	Archaeoglobus.				
OX	NCBI_TaxID=2234;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	SMRATN-VC-16 / DSM 4304 / ATCC 49558;				
RX	MEDLINE=98049343; PubMed=9389475;				
RA	Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,				
RA	Ketchum K.A., Dodson R.J., Gwin M., Hickey E.K., Peterson J.D.,				
RA	Richardson D.L., Kerlavage A.R., Graham D.E., Kyriades N.C.,				
RA	Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,				
RA	Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,				
RA	Peterson S., Retch C.L., McNeil L.K., Badger J.H., Glodex A., Zhou L.,				
RA	Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,				
RA	Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,				
RA	Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,				
RA	Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,				
RA	Venter J.C.;				
RT	"The complete genome sequence of the hyperthermophilic, sulphate-				
RT	reducing archaeon Archaeoglobus fulgidus.";				
RL	Nature 390:364-370(1997).				
CC	-I- SIMILARITY: STRONG, TO M.JANNASCHII MJ1678, M.THERMOAUTOTROPHICUM				
CC	MT1067 AND A.FULGIDUS AF0181.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; AE001105; AAB91200.1; -				
DR	TIGR; AF0028; -				
KM	Hypothetical protein.				
SO	SEQUENCE 371 AA; 41930 MW; B22056D00437BENA CRC64;				

Query Match 93.8%; Score 30; DB 1; Length 371;

Best Local Similarity 80.0%; Pred. No. 22;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDPLH 5
| | | | |
DB 56 HDFS 60

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RESULT 2
ID M1M_SALTY STANDARD: PRT: 307 AA.
AC P37168:
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE VIRULENCE FACTOR M1M.
GN M1M.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LT2 / KK1004:
RA van Slooten J.-C., Okada T., Kutsukake K., Pechere J.-C., Harayama S.;
RL Submitted (SEP-1993) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LT2:
RA MEDLINE=94259301; PubMed=8200538;
RX Kutsukake K., Okada T., Yokoseki T., Iino T.;
RT "Sequence analysis of the flag gene and its adjacent region in
RT Salmonella typhimurium, and identification of another flagellar gene,
RT flgN."
RL Gene 143:49-54(1994).
CC -1- SIMILARITY: TO E.COLI M1M.
-----
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL: 226133; GAB8133.1;
DR EMBL: D25292; BAA04981.1;
DR PIR: S40270; S40270.
DR StyGene: SG10239; mv1M.
DR InterPro: IPR000683;
DR Pfam: PF01408; GFO_IDH_MocA; 1.
DR Virulence.
FT CONFLICT 163 163 H -> D (IN REF. 2).
FT CONFLICT 194 194 G -> E (IN REF. 2).
SQ SEQUENCE 307 AA: 33958 MW: 35A60B55F27E6397 CRC64;

Query Match          90.6%; Score 29; DB 1; Length 307;
Best Local Similarity 80.0%; Pred. No. 29;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDPFH 5
DB 163 HDYLFH 167

RESULT 3
ID JAK2_MOUSE STANDARD: PRT: 1129 AA.
AC Q62120; Q62124;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TYROSINE-PROTEIN KINASE JAK2 (EC 2.7.1.112) (JANUS KINASE 2) (JAK-2).
GN JAK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=93391367; PubMed=8378315;
RA Silvenoinen O., Witthuhn B.A., Quelle F.W., Cleveland J.L., Yi T.,
RA Ihle J.N.;
RT "Structure of the murine Jak2 protein-tyrosine kinase and its role in
RT interleukin 3 signal transduction."
RL Proc. Natl. Acad. Sci. U.S.A. 90:8429-8433(1993).
RN [2]
RP SEQUENCE OF 973-1043 FROM N.A.
RX MEDLINE=90152381; PubMed=2482828;
RA Wilks A.F., Kurban R.R., Hovens C.M., Ralph S.J.;
RT "The application of the protein tyrosine kinase reaction to cloning members
RT of the protein tyrosine kinase family."
RL Gene 85:67-74(1989).
RN [3]
RP SEQUENCE OF 973-1043 FROM N.A.
RX MEDLINE=89160824; PubMed=2466296;
RA Wilks A.F.;
RT "Two putative protein-tyrosine kinases identified by application of
RT the polymerase chain reaction."
RL Proc. Natl. Acad. Sci. U.S.A. 86:1603-1607(1989).
CC -1- FUNCTION: TYROSINE KINASE OF THE NON-RECEPTOR TYPE, INVOLVED IN
CC INTERLEUKIN 3 SIGNAL TRANSDUCTION.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: WHOLLY INTRACELLULAR, POSSIBLY MEMBRANE
CC ASSOCIATED (BY SIMILARITY).
CC -1- DOMAIN: POSSESSES TWO PHOSPHOTRANSFERASE DOMAINS. THE SECOND ONE
CC PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHILE THE
CC PRESENCE OF SLIGHT DIFFERENCES SUGGEST A DIFFERENT ROLE FOR
CC DOMAIN 1.
CC -1- SIMILARITY: WITH NONRECEPTOR TYPE TYROSINE-PROTEIN KINASES.
CC BELONGS TO THE JANUS KINASES SUBFAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL: L16956; AAB41327.1;
DR EMBL: M33423; AAA40014.1;
DR HSSP: P11362; IFGI.
DR MGD: MGI:96629; Jak2.
DR InterPro: IPR000719;
DR InterPro: IPR000980;
DR InterPro: IPR001245;
DR Pfam: PF00069; Pkinase; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 2.
DR PROSITE: PS50001; SH2; UNKNOWN_1.
KW SH2 domain; Repeat.
FT DOMAIN 401 482 SH2 (ATYPICAL).
FT DOMAIN 545 809 PROTEIN KINASE 1.
FT NP_BIND 849 1124 PROTEIN KINASE 2.
FT BINDING 855 863 ATP (BY SIMILARITY).
FT ACT_SITE 882 882 ATP (BY SIMILARITY).
FT MOD_RES 976 976 BY SIMILARITY.
FT CONFLICT 1007 1007 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CONFLICT 1016 1016 S -> R (IN REF. 2 AND 3).
FT CONFLICT 1024 1024 Q -> E (IN REF. 2 AND 3).
FT CONFLICT 1042 1043 VV -> IP (IN REF. 2 AND 3).
SQ SEQUENCE 1129 AA: 130260 MW: 746CD480EB0A21B9 CRC64;

Query Match          90.6%; Score 29; DB 1; Length 1129;
Best Local Similarity 80.0%; Pred. No. 1,2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HDEFLH 5
 DB 159 HDEFLH 163

RESULT 4

JAK2_HUMAN STANDARD; PRT; 1132 AA.
 AC 060674; 075297; 014636;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE TYROSINE-PROTEIN KINASE JAK2 (EC 2.7.1.112) (JAKS KINASE 2) (JAK-2).
 GN JAK2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-98289582; PubMed-9618263;
 RA Saltman A., Stone M., Franks C., Searfoss G., Munro R., Jaye M.,
 RA Ivashchenko Y.;
 RT "Cloning and characterization of human Jak-2 kinase: high mRNA
 RT expression in immune cells and muscle tissue."
 RL Biochem. Biophys. Res. Commun. 246:627-633(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-98118198; PubMed-9446644;
 RA Dalal I., Arpaia E., Dadi H., Kulikarni S., Squite J., Rolfman C.M.;
 RT "Cloning and characterization of the human homolog of mouse Jak2.";
 RL Blood 91:844-851(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-97465498; PubMed-9326218;
 RA Peeters P., Raynaud S.D., Coils J., Wlodarska I., Grogg George J.,
 RA Philip P., Monpoux F., Van Rompaey L., Baens M., Van Den Bergh H.,
 RA Marynen P.;
 RT "Fusion of TEL, the ETS-variant gene 6 (ETV6), to the receptor-
 RT associated kinase JAK2 as a result of t(9;12) in a lymphoid and
 RT t(9;15;12) in a myeloid leukemia.";
 RL Blood 90:2535-2540(1997).
 CC -1- FUNCTION: TYROSINE KINASE OF THE NON-RECEPTOR TYPE, INVOLVED IN
 CC INTERLEUKIN 3 SIGNAL TRANSDUCTION.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: WHOLLY INTRACELLULAR, POSSIBLY MEMBRANE
 CC ASSOCIATED (BY SIMILARITY).
 CC -1- DOMAIN: POSSESSES TWO PHOSPHOTRANSFERASE DOMAINS. THE SECOND ONE
 CC PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHILE THE
 CC PRESENCE OF SLIGHT DIFFERENCES SUGGEST A DIFFERENT ROLE FOR
 CC DOMAIN 1.
 CC -1- DISEASE: A FORM OF PRE-B ACUTE MYELOID LEUKEMIA IS CHARACTERIZED
 CC BY A CHROMOSOMAL TRANSLOCATION T(9;12)(P24;P13) THAT INVOLVES
 CC ETV6 AND JAK2.
 CC -1- SIMILARITY: WITH NONRECEPTOR TYPE TYROSINE-PROTEIN KINASES.
 CC BELONGS TO THE JAKS KINASES SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: AF058925; AAC23982.1; -
 CC EMBL: AF001362; AAC23653.1; -
 CC EMBL: AF005216; AAB82092.1; -
 CC MIM: 147796; -
 CC InterPro: IPR000719; -
 CC InterPro: IPR000960; -
 CC InterPro: IPR001245; -

DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00069; pkinase; 2.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 2.
 DR PROSITE: PS50001; SH2; UNKNOWN_1.
 KW transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW SH2 domain; Repeat; Chromosomal translocation; Proto-oncogene.
 FT DOMAIN 401 482
 FT DOMAIN 545 809
 FT DOMAIN 849 1124
 FT NP_BIND 855 863
 FT BINDING 882 882
 FT ACT_SITE 976 976
 FT MOD_RES 1007 1007
 FT CONFLICT 321 321
 FT CONFLICT 1126 1126
 SQ SEQUENCE 1132 AA; 130673 MW; C3069EF1A7DA80C CRC64;

Query Match

Best Local Similarity 90.6%; Score 29; DB 1; Length 1132;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDEFLH 5
 DB 159 HDEFLH 163

RESULT 5

JAK2_RAT STANDARD; PRT; 1132 AA.
 AC 062689;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TYROSINE-PROTEIN KINASE JAK2 (EC 2.7.1.112) (JAKS KINASE 2) (JAK-2).
 GN Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-9531631; PubMed-760755;
 RA Dubé R.J., Rui H., Greenwood J.D., Garvey K., Farrar M.L.;
 RT "Cloning of the gene encoding rat JAK2, a protein tyrosine kinase.";
 RL Gene 158:281-285(1995).
 CC -1- FUNCTION: TYROSINE KINASE OF THE NON-RECEPTOR TYPE, INVOLVED IN
 CC INTERLEUKIN 3 SIGNAL TRANSDUCTION.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: WHOLLY INTRACELLULAR, POSSIBLY MEMBRANE
 CC ASSOCIATED (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: HIGHLY ABUNDANT IN BRAIN AND SPLEEN, LESS
 CC ABUNDANT IN SKELETAL MUSCLE AND TESTIS, AND DETECTABLE IN KIDNEY,
 CC HEART, LUNG AND LIVER.
 CC -1- DOMAIN: POSSESSES TWO PHOSPHOTRANSFERASE DOMAINS. THE SECOND ONE
 CC PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHILE THE
 CC PRESENCE OF SLIGHT DIFFERENCES SUGGEST A DIFFERENT ROLE FOR
 CC DOMAIN 1.
 CC -1- SIMILARITY: WITH NONRECEPTOR TYPE TYROSINE-PROTEIN KINASES.
 CC BELONGS TO THE JAKS KINASES SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: U13396; AAA79911.1; -

DR HSSE; P11362; IFC1.
 DR InterPro: IPR000719; .
 DR InterPro: IPR000980; .
 DR InterPro: IPR001245; .
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00069; pkinase; 2.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 2.
 DR PROSITE: PS00001; SH2; UNKNOWN; 1.
 KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW SH2 domain; Repeat.
 FT DOMAIN 401 482 SH2 (ATYPICAL).
 FT DOMAIN 545 809 PROTEIN KINASE 1.
 FT DOMAIN 849 1126 PROTEIN KINASE 2.
 FT NP_BIND 855 863 ATP (BY SIMILARITY).
 FT BINDING 882 882 ATP (BY SIMILARITY).
 FT ACT_SITE 976 976 BY SIMILARITY.
 FT MOD_RES 1007 1007 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 1132 AA; 130585 MW; 3AEDF2PECE8B95A CRC64;

Query Match 90.6%; Score 29; DB 1; Length 1132;
 Best Local Similarity 80.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDEFLH 5
 |||||
 DB 159 HDEFLH 163

RESULT 6
 YGEL_YEAST STANDARD; PRT; 104 AA.
 AC P53182; 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPOTHETICAL 12.0 KDA PROTEIN IN DST1-HEM2 INTERGENIC REGION.
 GN YGL041C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C;
 RA MEDLINE-97377993; PubMed=9234674;
 RA Feuerhann M., de Montigny J., Potier S., Souciet J.-L.;
 RT "The characterization of two new clusters of duplicated genes
 RT suggests a 'leugo' organization of the yeast Saccharomyces cerevisiae
 RT chromosomes".
 RT Yeast 13:861-869(1997).
 RN [2]
 RP SEQUENCE OF 18-104 FROM N.A.
 RA Hedling U., Hofmann B., Delius H.;
 RT Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
 CC -----
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 CC -----
 CC EMBL; 272563; CAA96743.1; .
 DR SGD; S0003009; YGL041C.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 19 39 POTENTIAL.
 FT TRANSMEM 68 88 POTENTIAL.
 SQ SEQUENCE 104 AA; 11977 MW; 85A3E9FC9A7AD93 CRC64;

Query Match 87.5%; Score 28; DB 1; Length 104;
 Best Local Similarity 80.0%; Pred. No. 15;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDEFLH 5
 |||||
 DB 70 HDEFLH 74

RESULT 7
 RISB_BRUAB STANDARD; PRT; 158 AA.
 AC Q4468; 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE 6,7-DIMETHYL-8-RIBITYLUMAZINE SYNTHASE (EC 2.5.1.9) (DMRL SYNTHASE)
 DE (LUMAZINE SYNTHASE) (RIBOFLAVIN SYNTHASE BETA CHAIN).
 GN RIBH.
 OS Brucella abortus.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=235;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-95393285; PubMed=7664168;
 RA Hemmen F., Weynants V., Scarcez T., Letesson J., Saman E.;
 RT "Cloning and sequence analysis of a newly identified Brucella abortus
 RT gene and serological evaluation of the 17-kilodalton antigen that it
 RT encodes".
 RT Clin. Diagn. Lab. Immunol. 2:263-267(1995).
 CC -!- FUNCTION: RIBOFLAVIN SYNTHASE IS A BIFUNCTIONAL ENZYME COMPLEX
 CC CATALYZING THE FORMATION OF RIBOFLAVIN FROM 5-AMINO-6-(1'-D)-
 CC RIBITYL-AMINO-2,4(1H,3H)-PYRIMIDINEDIONE AND L-3,4-DIHYDRO-2-
 CC BUTANONE-4-PHOSPHATE VIA 6,7-DIMETHYL-8-LUMAZINE. THE BETA
 CC SUBUNIT CATALYZES THE CONDENSATION OF 5-AMINO-6-(1'-D)-RIBITYL-
 CC AMINO-2,4(1H,3H)-PYRIMIDINEDIONE WITH L-3,4-DIHYDRO-2-BUTANONE-
 CC 4-PHOSPHATE YIELDING 6,7-DIMETHYL-8-LUMAZINE (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: 2 6,7-DIMETHYL-8-(1-D-RIBITYL)LUMAZINE -
 CC RIBOFLAVIN + 4-(1-D-RIBITYLAMINO)-5-AMINO-2,6-DIHYDROXYPYRIMIDINE.
 CC -!- COFACTOR: FLAVOPROTEIN (BY SIMILARITY).
 CC -!- PATHWAY: FINAL STEP OF RIBOFLAVIN SYNTHESIS.
 CC -!- SUBUNIT: OLIGOMER THAT CONSIST OF 3 ALPHA SUBUNITS AND 60 BETA
 CC SUBUNITS (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE DMRL SYNTHASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; 246864; CAA86936.1; .
 DR Pfam: PF00885; DMRL_synthase; 1.
 KW Riboflavin biosynthesis; transferase; Flavoprotein.
 SQ SEQUENCE 158 AA; 17356 MW; EE59C2815E33A2B CRC64;

Query Match 87.5%; Score 28; DB 1; Length 158;
 Best Local Similarity 80.0%; Pred. No. 23;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 HDEFLH 5
 |||||
 DB 126 HDEFLH 130

RESULT 8
 YE99_MYCPN STANDARD; PRT; 163 AA.
 ID YE99_MYCPN


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AC p75288;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE HYPOThETICAL PROTEIN MPN499 (P02_ORF163).
GN MPN499 OR MP344.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RA MEDLINE=97105885; PubMed=8948633;
RA Himmelfreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
RA Hermann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae."
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -----
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CC -----
CC EMBL: AE000032; AAB95991.1; -.
KW Hypothetical protein.
SQ SEQUENCE 163 AA; 19095 MW; 10CE2D2F077DFEAC CRC64;

Query Match      87.5%; Score 28; DB 1; Length 163;
Best Local Similarity 80.0%; Pred. No. 24;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 HDELH 5
Db 72 HDEFFH 76

RESULT 9
Y038_NPVOP
ID Y038_NPVOP STANDARD; PRT; 209 AA.
OC 005125; 010283;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE HYPOThETICAL 24.3 KDA PROTEIN (ORF22) (ORF 7).
OS Orygia pseudotsugata multicapsid polyhedrosis virus (OPMNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10450;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97271300; PubMed=9126251;
RA Ahrens C.H., Russell R.R., Funk C.J., Evans J., Haywood S.,
RA Rohmann G.F.;
RT "The sequence of the Orygia pseudotsugata multinucleocapsid nuclear
RT polyhedrosis virus genome."
RL Virology 229:381-399(1997).
RN [2]
RP SEQUENCE OF 30-209 FROM N.A.
RX MEDLINE=93286576; PubMed=8389803;
RA Russell R.L.O., Rohmann G.F.;
RT "Nucleotide sequence of the ubiquitin-39K gene region from the Orygia
RT pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome."
RL J. Gen. Virol. 74:1191-1195(1993).
CC -1- SIMILARITY: TO CORRESPONDING ORF IN ACMNPV.
CC -----
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CC -----
CC EMBL: U75930; AAC59021.1; -.
DR EMBL: D13375; BAA02636.1; -.
KW Hypothetical protein.
FT CONFLICT 35
SQ SEQUENCE 209 AA; 24253 MW; C344C51CB9F78D66 CRC64;

Query Match      87.5%; Score 28; DB 1; Length 209;
Best Local Similarity 80.0%; Pred. No. 31;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 HDELH 5
Db 186 HDEFFH 190

RESULT 10
BZTD_RHOCA
ID BZTD_RHOCA STANDARD; PRT; 263 AA.
AC 052666;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE GLUTAMATE/GLUTAMINE/ASPARTATE/ASPARAGINE TRANSPORT ATP-BINDING PROTEIN
DE BZTD.
GN BZTD.
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SB1003 / ST LOUIS;
RX MEDLINE=96405624; PubMed=8809753;
RA Zheng S., Haselkorn R.;
RT "A glutamate/glutamine/aspartate/asparagine transport operon in
RT Rhodobacter capsulatus."
RL Mol. Microbiol. 20:1001-1011(1996).
CC -1- FUNCTION: PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM FOR
CC GLUTAMATE, GLUTAMINE, ASPARTATE, ASPARAGINE. PROBABLY RESPONSIBLE
CC FOR ENERGY COUPLING TO THE TRANSPORT SYSTEM.
CC -1- SUBUNIT: BZTB AND BZTC FORM A HETERODIMER WHICH CAN FORM A
CC MEMBRANE COMPLEX WITH A HOMODIMER OF BZTD (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
CC (ABC TRANSPORTERS).
CC -----
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CC -----
CC EMBL: U37407; AAB1789.1; -.
DR Interpro: IPR001617; -.
DR Pfam: PF00005; ABC_tran. 1.
DR PROSITE: PS00211; ABC_TRANSPORTER. 1.
KW Amino-acid transport; Transport; ATP-binding.
FT NP_BIND 55
SQ SEQUENCE 263 AA; 30012 MW; A08DF5ABE6A4498D CRC64;

Query Match      87.5%; Score 28; DB 1; Length 263;
Best Local Similarity 80.0%; Pred. No. 40;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 HDELH 5
1111
DB 242 HDELH 246

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RESULT 11
TREC_ECOLI STANDARD: PRT: 551 AA.
AC P28904;
DT 01-DEC-1992 (rel. 24, Created)
DT 01-FEB-1995 (rel. 31, Last sequence update)
DT 30-MAY-2000 (rel. 39, Last annotation update)
DE TREHALOSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.93) (ALPHA, ALPHA-
DE PHOSPHOTREHALASE).
GN TREC OR OLGH.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=94364944; PubMed=8083158;
RA Rimmel M., Boos W.;
RT "Trehalose-6-phosphate hydrolase of Escherichia coli.";
RL J. Bacteriol. 176:5654-5664(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=95334362; PubMed=7610040;
RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RA Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
RT region from 92.8 through 100 minutes.";
RL Nucleic Acids Res. 23:2105-2119(1995).
RN [3]
RP SEQUENCE OF 160-392 FROM N.A.
RC STRAIN=K12 / W3110;
RX MEDLINE=93133831; PubMed=8421692;
RA Sun X., Harder J., Krook M., Joernvall H., Sjoberg B.-M.,
RA Reichard P.;
RT "A possible glycine radical in anaerobic ribonucleotide reductase
RT from Escherichia coli: nucleotide sequence of the cloned nrdp gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:577-581(1993).
RN [4]
RP -1- CATALYTIC ACTIVITY: ALPHA, ALPHA-TREHALOSE 6-PHOSPHATE + H(2)O =
CC D-GLUCOSE + D-GLUCOSE 6-PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC -----
CC EMBL: U06195; AAC3382.1; -
CC EMBL: U14003; AAA97136.1; -
CC EMBL: AE000495; AAC71196.1; -
CC EMBL: L06097; AAA24225.1; -
CC Ecocore: EG11402; trec.
CC InterPro: IPR000461; -
CC Pfam: PF00128; alpha-amylase; 1.
CC Hydrolase; Glycosidase.
CC ACT_SITE 200 200 BY SIMILARITY.
CC ACT_SITE 251 251 BY SIMILARITY.
CC ACT_SITE 325 325 BY SIMILARITY.
CC CONFLICT 74 74 D -> V (IN REF. 1).
CC SEQUENCE 551 AA; 63837 MW; 975F89FBD91621A6 CRC64;
```

Query Match 87.5%; Score 28; DB 1; Length 551;
Best Local Similarity 80.0%; Pred. No. 89;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDELH 5
1:111
DB 230 HDELH 234

```
RESULT 12
TREC_BACSU STANDARD: PRT: 561 AA.
ID TREC_BACSU
AC P39795; O34517;
DT 01-FEB-1995 (rel. 31, Created)
DT 30-MAY-2000 (rel. 39, Last sequence update)
DT 30-MAY-2000 (rel. 39, Last annotation update)
DE TREHALOSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.93) (ALPHA, ALPHA-
DE PHOSPHOTREHALASE).
GN TREA OR TREC.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / MARBURG;
RX MEDLINE=95379486; PubMed=7651129;
RA Helvert C., Gotsche S., Dahl M.K.;
RT "Cleavage of trehalose-phosphate in Bacillus subtilis is catalysed by
RT a phospho-alpha-(1-1)-glucosidase encoded by the trea gene.";
RL Mol. Microbiol. 16:111-120(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AC327;
RX MEDLINE=97124190; PubMed=8969503;
RA Yamamoto H., Uchiyama S., Sekiguchi J.;
RT "Cloning and sequencing of a 40.6 kb segment in the 73 degrees-76
RT degrees region of the Bacillus subtilis chromosome containing genes
RT for trehalose metabolism and acetoin utilization.";
RL Microbiology 142:3057-3065(1996).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=95270588; PubMed=7751281;
RA Gotsche S., Dahl M.K.;
RT "Purification and characterization of the phospho-
RT alpha(1,1)glucosidase (Trea) of Bacillus subtilis 168.";
RL J. Bacteriol. 177:2721-2726(1995).
RN [4]
RP -1- CATALYTIC ACTIVITY: ALPHA, ALPHA-TREHALOSE 6-PHOSPHATE + H(2)O =
CC D-GLUCOSE + D-GLUCOSE 6-PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC -----
CC EMBL: 254245; CAA91015.1; -
CC EMBL: X80203; CAA56495.1; -
CC EMBL: D83967; BAA23408.1; -
CC EMBL: 299108; CAB12610.1; -
CC HSSP: P21332; 100K.
CC Subtilist: BG11010; trea.
CC InterPro: IPR000461; -
CC Pfam: PF00128; alpha-amylase; 1.
CC Hydrolase; Glycosidase.
CC ACT_SITE 203 203 BY SIMILARITY.
CC ACT_SITE 254 254 BY SIMILARITY.
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```
FT ACT_SITE 329 329 BY SIMILARITY.
FT CONFLICT 114 123 FREAUSSIDS -> LRGDLFNRQ (IN REF. 1).
FT CONFLICT 196 196 G -> E (IN REF. 1).
FT CONFLICT 288 290 PNG -> LRA (IN REF. 1).
FT CONFLICT 386 386 V -> A (IN REF. 1).
FT CONFLICT 547 561 LRPESIVYRLTKPC -> VAIMSPLEIV (IN REF. 1).
SQ SEQUENCE 561 AA; 65183 MW; 12C0AC7F069139A5 CRC64;

Query Match 87.5%; Score 28; DB 1; Length 561;
Best Local Similarity 80.0%; Pred. No. 90;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDEFLH 5
Db 233 HEFLH 237

RESULT 13
ID MEPR_HUMAN STANDARD; PRT; 700 AA.
AC 016820;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE MEPRIN A BETA-SUBUNIT PRECURSOR (EC 3.4.24.18) (ENDOPEPTIDASE-2) (N-
DE BENZOYL-L-TYROSYL-P-AMINO-BENZOIC ACID HYDROLASE BETA SUBUNIT) (PABA
DE PEPTIDE HYDROLASE) (PPH BETA).
GN MEPRB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Jejunum;
RA Eiderling J.A., Groenbergh J., Sterchi E.E.;
RL Submitted (Oct-1994) to the EMBL/Genbank/DDb databases.
CC -1 CATALYTIC ACTIVITY: HYDROLYSIS OF PROTEIN AND PEPTIDE SUBSTRATES
CC -1 PREFERENTIALLY ON CARBOXYL SIDE OF HYDROPHOBIC RESIDUES.
CC -1 CORFACTOR: BINDS ONE ZINC ION.
CC -1 SUBUNIT: HOMOTETRAMER OF ALPHA OR BETA SUBUNITS; HETEROTETRAMER
CC OF TWO ALPHA AND TWO BETA SUBUNITS ARE FORMED BY NON-COVALENT
CC ASSOCIATION OF TWO DISULFIDE-LINKED HETERODIMERS (BY SIMILARITY).
CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC
CC METALLOPROTEASE); ALSO KNOWN AS THE ASTACTIN SUBFAMILY.
CC -1 SIMILARITY: CONTAINS 1 MAM DOMAIN.
CC -1 SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X81333; CAA57107.1; -.
CC HSSP: P28825; IIAF.
CC MEROPS: M12.004; -.
CC MIM: 600389; -.
CC InterPro: IPR000130; -.
CC InterPro: IPR000561; -.
CC InterPro: IPR000998; -.
CC InterPro: IPR001506; -.
CC InterPro: IPR002083; -.
CC Pfam: PF01400; Astactin; 1.
CC Pfam: PF00629; MAM; 1.
CC Pfam: PF00917; MATH; 1.
CC PRINTS: PR00020; MAMDOMAIN.
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DR PRINTS: PR00480; ASTACTIN
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
DR PROSITE: PS00740; MAM_1; 1.
DR PROSITE: PS50060; MAM_2; 1.
DR PROSITE: PS00022; EGF_1; FALSE_NEG.
DR PROSITE: PS01186; EGF_2; FALSE_NEG.
KW Transmembrane; Hydrolase; Metalloprotease; Zinc; Glycoprotein;
KW Zymogen; Signal; EGF-like domain.
FT SIGNAL 1 22
FT PROPEP 23 63 BY SIMILARITY.
FT CHAIN 64 700 MEPRIN A BETA-SUBUNIT.
FT DOMAIN 23 652 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 653 673 POTENTIAL.
FT DOMAIN 674 700 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 64 259 METALLOPROTEASE.
FT DOMAIN 260 429 MAM.
FT DOMAIN 604 644 EGF-LIKE.
FT METAL 152 152 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 153 153 BY SIMILARITY.
FT METAL 156 156 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 162 162 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 608 619 BY SIMILARITY.
FT DISULFID 613 628 BY SIMILARITY.
FT DISULFID 630 643 BY SIMILARITY.
FT CARBOHYD 218 218 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 370 370 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 421 421 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 436 436 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 547 547 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 592 592 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 700 AA; 79459 MW; F7C7D728A4E3B32 CRC64;

Query Match 87.5%; Score 28; DB 1; Length 700;
Best Local Similarity 80.0%; Pred. No. 1; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDEFLH 5
Db 152 HEFLH 156

RESULT 14
ID MEPR_MOUSE STANDARD; PRT; 704 AA.
AC 061847;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE MEPRIN A BETA-SUBUNIT PRECURSOR (EC 3.4.24.18) (ENDOPEPTIDASE-2).
GN MEPRB OR MEPR-1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Kidney;
RC MEDLINE=94012651; PubMed=8407940;
RX Gorbea C.M., Marchand P., Jiang W., Copeland N.G., Gilbert D.J.,
RX Jenkins N.A., Bond J.S.;
RT "Cloning, expression, and chromosomal localization of the mouse
RT meprin beta subunit."
RL J. Biol. Chem. 268:21035-21043(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM BETA').
RC TISSUE=Kidney;
RX MEDLINE=96147211; PubMed=8567689;
RX Dietrich J.M., Bond J.S., Jiang W.,
RX "A novel meprin beta mRNA in mouse embryonal and human colon
RX carcinoma cells.";
```

RL J. Biol. Chem. 271:2271-2278(1996).
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF PROTEIN AND PEPTIDE SUBSTRATES
 CC PREFERENTIALLY ON CARBOXYL SIDE OF HYDROPHOBIC RESIDUES.
 CC -1- COFACTOR: BINDS ONE ZINC ION.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA AND TWO BETA SUBUNITS WHICH
 CC IS FORMED BY THE NON-COVALENT ASSOCIATION OF TWO DISULFIDE-LINKED
 CC HETERODIMERS.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, THE BETA AND BETA' SUBUNITS,
 CC DIFFER IN THEIR N-TERMINUS DUE TO DIFFERENTIAL PROMOTER USAGE AND
 CC ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: THE BETA-SUBUNIT IS EXPRESSED IN KIDNEY.
 CC -1- INTESTINAL BRUSH BORDERS, AND SALIVARY DUCTS. THE BETA'-ISOFORM
 CC HAS BEEN FOUND IN CARCINOMA CELLS.
 CC -1- INDUCTION: THE BETA'-SUBUNIT IS INDUCED BY THE MORPHOGEN RETINOIS
 CC ACID.
 CC -1- PTM: THIS PROTEIN UNDERGOES PROTEOLYTIC PROCESSING. BOTH FORMS
 CC ARE GLYCOSYLATED.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC
 CC METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -----
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 CC -----
 CC EMBL: L15193; AAA75234.1; -
 CC DR HSSP: P28825; 11AF.
 CC DR MEROPS: M12.002; -
 CC DR MEROPS: M12.004; -
 CC DR MGD: MGI:96964; Mep1b.
 CC DR InterPro: IPR000130; -
 CC DR InterPro: IPR000561; -
 CC DR InterPro: IPR000998; -
 CC DR InterPro: IPR001506; -
 CC DR InterPro: IPR002083; -
 CC DR Pfam: PF01400; Astacin; 1.
 CC DR Pfam: PF00008; EGF; 1.
 CC DR Pfam: PF00629; MAM; 1.
 CC DR Pfam: PF00917; MATN; 1.
 CC DR PRINTS: PR00020; MAMDOMAIN.
 CC DR PRINTS: PR00480; ASTACIN.
 CC DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 CC DR PROSITE: PS00740; MAM_1; 1.
 CC DR PROSITE: PS00600; MAM_2; 1.
 CC DR PROSITE: PS00022; EGF_1; FALSE_NEG.
 CC DR PROSITE: PS01186; EGF_2; FALSE_NEG.
 CC KM Transmembrane: Hydrolase; Metalloprotease; Zinc; Glycoprotein;
 CC KMGlycogen: Signal; EGF-like domain; Alternative splicing.
 CC SIGNAL 1 20
 CC PROPEP 21 64
 CC CHAIN 65 704
 CC DOMAIN 21 654
 CC TRANSMEM 655 678
 CC DOMAIN 679 704
 CC DOMAIN 63 260
 CC DOMAIN 261 430
 CC DOMAIN 607 647
 CC METAL 153 153
 CC METAL 154 154
 CC ACT_SITE 157 157
 CC METAL 163 163
 CC METAL 611 622
 CC DISULFID 616 631
 CC DISULFID 633 646
 CC CARBOHYD 193 193
 CC CARBOHYD 219 219
 CC CARBOHYD 255 255

FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 422 422 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 437 437 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 529 529 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 548 548 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 593 593 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 1 27 MDAHQPWFLVFATLVLASGLAPAKE -> MNSGAPASR
 FT SRSFRCRKLKLRKAPDCMYMTFG (IN ISOFORM
 FT BETA').
 SQ SEQUENCE 704 AA; 79548 MW; 2D610FDD74650F70 CRC64;
 QY 1 HDRLH 5
 DB 153 HDRLH 157
 Query Match 87.5%; Score 28; DB 1; Length 704;
 Best Local Similarity 80.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 RESULT 15
 MEPR_RAT STANDARD; PRT; 704 AA.
 ID MEPR_RAT
 AC P28826;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE MEPRIN A BETA-SUBUNIT PRECURSOR (EC 3.4.24.18) (ENDOPEPTIDASE-2).
 GN MEPRB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Kidney;
 RA MEDLINE=92317075; PubMed=1377685;
 RX Johnson G.D., Hersch L.B.;
 RT "Cloning a rat meprin cDNA reveals the enzyme is a heterodimer";
 RL J. Biol. Chem. 267:13505-13512(1992).
 RN [2]
 RP ERRATUM (RETRACTION).
 RX MEDLINE=93359474; PubMed=8354669;
 RA Johnson G.D., Hersch L.B.;
 RL J. Biol. Chem. 268:17647-17647(1993).
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF PROTEIN AND PEPTIDE SUBSTRATES
 CC PREFERENTIALLY ON CARBOXYL SIDE OF HYDROPHOBIC RESIDUES.
 CC -1- COFACTOR: BINDS ONE ZINC ION.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA AND TWO BETA SUBUNITS WHICH
 CC IS FORMED BY THE NON-COVALENT ASSOCIATION OF TWO DISULFIDE-LINKED
 CC HETERODIMERS.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: KIDNEY, INTESTINAL BRUSH BORDERS, AND
 CC SALIVARY DUCTS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC
 CC METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M88601; AAA41587.1; -
 CC PIR: A42908; A42908.
 CC HSSP: P28825; 11AF.
 CC MEROPS: M12.002; -
 CC MEROPS: M12.004; -
 CC InterPro: IPR000130; -

DR InterPro; IPR000561; -;
 DR InterPro; IPR000998; -;
 DR InterPro; IPR001506; -;
 DR InterPro; IPR002083; -;
 DR pfam; PF01400; Astacin; 1.
 DR pfam; PF00629; MAM; 1.
 DR pfam; PF00917; MATH; 1.
 DR PRINTS; PR00020; MAMDOMAIN.
 DR PRINTS; PR00480; ASTACIN.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 DR PROSITE; PS00740; MAM_1; 1.
 DR PROSITE; PS50060; MAM_2; 1.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 KW Transmembrane; Hydrolase; Metalloprotease; Zinc; Glycoprotein;
 KW Zymogen; Signal; EGF-like domain.
 FT SIGNAL 1 20 POTENTIAL.
 FT PROPEP 21 64
 FT CHAIN 65 704 MEPRIN A BETA-SUBUNIT.
 FT DOMAIN 21 654 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 655 678 POTENTIAL.
 FT DOMAIN 679 704 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 63 260 METALLOPROTEASE.
 FT DOMAIN 261 430 MAM.
 FT DOMAIN 607 647 EGF-LIKE.
 FT METAL 153 153 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT_SITE 154 154 BY SIMILARITY.
 FT METAL 157 157 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 163 163 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 163 163 BY SIMILARITY.
 FT DISULFID 611 622 BY SIMILARITY.
 FT DISULFID 616 631 BY SIMILARITY.
 FT DISULFID 633 646 BY SIMILARITY.
 FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 219 219 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 422 422 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 437 437 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 528 528 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 547 547 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 592 592 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 704 AA; 79249 MW; 1FBC21129EC6B875 CRC64;

Query Match 87.5%; Score 28; DB 1; Length 704;
 Best Local Similarity 80.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDEFLH 5
 1:111
 DB 153 HDEFLH 157

Search completed: August 9, 2001, 20:36:50
 Job time: 699 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 9, 2001, 20:24:14 ; Search time 79.24 seconds
(without alignments)
3.825 Million cell updates/sec

Title: US-09-367-013b-2_COPY_39_43
Perfect score: 26
Sequence: 1 KVPDV 5

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: /SIDSR/gcgcdata/geneseq/geneseq/AA1981.DAT.*
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9: /SIDSR/gcgcdata/geneseq/geneseq/AA1988.DAT.*
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21: /SIDSR/gcgcdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDSR/gcgcdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	60	21	AA18359
2	26	100.0	78	21	AA27099
3	26	100.0	79	21	AA35333
4	26	100.0	90	21	AA38087
5	26	100.0	95	21	AA19062
6	26	100.0	96	21	AA28353
7	26	100.0	104	21	AA24812
8	26	100.0	104	21	AA18358
9	26	100.0	104	21	AA44772
10	26	100.0	116	21	AA32671
11	26	100.0	120	21	AA11409

12	26	100.0	126	21	AA23318	Arabidopsis thalia
13	26	100.0	129	21	AA25659	Arabidopsis thalia
14	26	100.0	134	21	AA20798	Arabidopsis thalia
15	26	100.0	135	21	AA23317	Arabidopsis thalia
16	26	100.0	136	21	AA20776	Arabidopsis thalia
17	26	100.0	136	21	AA24993	Arabidopsis thalia
18	26	100.0	138	21	AA28352	Arabidopsis thalia
19	26	100.0	140	21	AA24685	Arabidopsis thalia
20	26	100.0	140	21	AA23798	Arabidopsis thalia
21	26	100.0	140	21	AA24407	Arabidopsis thalia
22	26	100.0	151	21	AA24761	Plant SDF encoded
23	26	100.0	151	21	AA24809	Plant SDF encoded
24	26	100.0	151	21	AA24830	Plant SDF encoded
25	26	100.0	151	21	AA24941	Plant SDF encoded
26	26	100.0	151	21	AA24247	Arabidopsis thalia
27	26	100.0	151	21	AA28091	Arabidopsis thalia
28	26	100.0	155	21	AA28571	Arabidopsis thalia
29	26	100.0	164	21	AA44213	Rice phytoene synth
30	26	100.0	166	21	AA28351	Arabidopsis thalia
31	26	100.0	181	21	AA28086	Arabidopsis thalia
32	26	100.0	195	21	AA24811	Plant SDF encoded
33	26	100.0	195	21	AA24771	Arabidopsis thalia
34	26	100.0	200	21	AA24861	Arabidopsis thalia
35	26	100.0	241	21	AA25493	Arabidopsis thalia
36	26	100.0	254	19	AA21987	Flea serine protea
37	26	100.0	254	22	AA25067	Arabidopsis thalia
38	26	100.0	325	21	AA28976	Arabidopsis thalia
39	26	100.0	325	21	AA26647	Arabidopsis thalia
40	26	100.0	349	20	AA209298	Rice beta-glucanase
41	26	100.0	377	20	AA209306	Rice Gm9 CDS prot
42	26	100.0	410	19	AA21059	Phytoene synthase
43	26	100.0	425	19	AA26962	Amino acid sequenc
44	26	100.0	426	19	AA26961	Amino acid sequenc
45	26	100.0	428	19	AA26963	Amino acid sequenc

ALIGNMENTS

RESULT 1	
ID	AA18359 standard; Protein: 60 AA.
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AC	AA18359;
XX	
DT	17-OCT-2000 (first entry)
XX	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 19732.
XX	
KW	Protein identification; signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter;
KW	termination sequence.
XX	
OS	Arabidopsis thaliana.
XX	
PN	EP1033405-A2.
XX	
PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 2000EP-0301439.
XX	
PR	25-FEB-1999; 99US-0121825.
PR	05-MAR-1999; 99US-0123180.
PR	09-MAR-1999; 99US-0123548.
PR	23-MAR-1999; 99US-0125788.
PR	25-MAR-1999; 99US-0126264.
PR	29-MAR-1999; 99US-0126785.
PR	01-APR-1999; 99US-0127462.
PR	06-APR-1999; 99US-0128234.
PR	08-APR-1999; 99US-0128714.
PR	16-APR-1999; 99US-0129845.
PR	19-APR-1999; 99US-0130077.
PR	21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
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Query Match 100.0%; Score 26; DB 21; Length 60;
Best Local Similarity 100.0%; Pred. No. 22;
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Db 5 kvdv 9

RESULT 2

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ID AAG27099 standard; Protein: 78 AA.

AC AAG27099;

DT 17-OCT-2000 (first entry)

DE Zea mays protein fragment SEQ ID NO: 31805.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corr.

OS Zea mays subsp. mays.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

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Query Match 100.0%; Score 26; DB 21; Length 78;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKYDV 5
Db 29 kkydv 33

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ID AACG35333 standard; Protein; 79 AA.
XX AC AACG35333;
XX DT 18-OCT-2000 (first entry)
XX DE Zea mays protein fragment SEQ ID NO: 43147.
XX Zea mays protein fragment SEQ ID NO: 43147.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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Query Match 100.0%; Score 26; DB 21; Length 95;
Best Local Similarity 100.0%; Pred. No. 37;
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Db 29 kyydv 33

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AAG28353
ID AAG28353 standard; Protein; 96 AA.

XX AAG28353;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 33539.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

XX EPI033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

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PR 29-OCT-1999; 99US-0162142.

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Query Match      100.0%; Score 26; DB 21; Length 96;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 KYVDV 5
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DB 41 kydv 45

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RESULT 7
ID AAB24812 standard; Peptide: 104 AA.

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XX AAB24812;
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XX 27-NOV-2000 (first entry)
DT
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XX Plant SDF encoded polypeptide sequence SEQ list 1 NO:292.
DE
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XX Plant: corn; Arabidopsis thaliana; sequence-determined DNA fragment;
KW SDF; genetic mapping; identification; promoter; structural gene; UTR;
KM untranslated region; expression control.
XX
XX Plant.
OS
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XX WO200040695-A2.
XX
XX 13-JUL-2000.
XX
XX 07-JAN-2000; 2000MO-US00466.
XX
XX 08-JAN-1999; 99US-0115293.
XX
XX (CERE-) CERES INC.
XX
XX Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L;
XX
XX WPI; 2000-465970/40.
XX
XX New corn plant and Arabidopsis thaliana sequence-determined DNA
PT fragments, useful for expressing gene products and for controlling
PT expression of a target gene -
XX
XX
PS Claim 14; Page 464; 673pp; English.
XX
XX The present invention describes polynucleotides, such as complete cDNA
CC sequences and/or sequences of genomic DNA encompassing complete genes,
CC portions of genes, and/or intergenic regions, collectively referred to
CC as sequence-determined DNA fragments (SDFs), from corn plants and
CC Arabidopsis thaliana. The SDFs are promoters, structural genes,
CC untranslated regions (UTRs), or 3' termination sequences. They can be
CC used for expressing a gene product and controlling expression of a
CC target gene, either as a promoter, a structural gene, an UTR or as a
CC 3' termination sequence. They are also useful as tools for genetic
CC mapping, and identification of a particular individual plant or for
CC clustering a group of plants with a common trait. AAB78433 to AAB78630
CC and AAB24605 to AAB25099 represent the specifically claimed
CC polynucleotide sequences and polypeptides encoded by them given in the
CC present invention.
XX
XX Sequence 104 AA;
SQ

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Query Match      100.0%; Score 26; DB 21; Length 104;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AC AAG18358;
AC
XX
XX 17-OCT-2000 (first entry)
DT
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 19731.

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XX protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
KW

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KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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Best Local Similarity 100.0%; Pred. NO. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 9

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ID AAG44772 standard; Protein; 104 AA.

AC AAG44772;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 56122.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

XX EPI033405-A2.

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Query Match 100.0%; Score 26; DB 21; Length 104;
Best Local Similarity 100.0%; Pred. No. 41;
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Db 5 kvpdv 9

RESULT 10

AAG32671
ID AAG32671 standard; Protein: 116 AA.

XX AAG32671;

XX 17-OCT-2000 (first entry)

DE Zea mays protein fragment SEQ ID NO: 39459.

XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.

XX OS Zea mays subsp. mays.

XX PN EPI033405-A2.

XX PD 06-SEP-2000.

PE 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

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PR 29-OCT-1999; 99US-0162142.

Query Match 100.0%; Score 26; DB 21; Length 116;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVDY 5
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DB 29 kvdyv 33

RESULT 11

ID AAB11409 standard; Protein; 120 AA.
XX AAB11409;
XX
XX 22-FEB-2001 (first entry)
XX
XX S. cerevisiae cytochrome b5 protein.
XX
XX Cytochrome b5; alkane metabolism; oxidation; long-chain alkyl compound;
XX
XX Long-chain dicarboxylic acid.
XX
XX Saccharomyces cerevisiae.
XX
XX WO200065061-A2.
XX
XX 02-NOV-2000.
XX
XX 18-APR-2000; 2000WO-DE01246.
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XX 24-APR-1999; 99DE-1018763.
XX
XX
XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
XX Schunck W, Chernogolov A;
XX
XX WPI; 2000-679674/66.
XX
XX Nucleic acid sequences from alkane metabolizing Candida yeast, encoding
XX
XX cytochrome b5 and used for the oxidation of long chain alkyl compounds
XX
XX and for the production of long chain dicarboxylic acids -

PS Example 1.4; Fig 2a; 27pp; German.

XX
XX This invention describes novel nucleic acid sequences from alkane
CC metabolizing Candida yeasts, encoding cytochrome b5-polypeptide, its
CC fragments, variants and mutations. The nucleic acids and polypeptides
CC are used for the oxidation of long-chain alkyl compounds with at least
CC 10C, and for the production of long-chain dicarboxylic acids by oxidizing
CC n-alkanes and fatty acids with at least 10C.
XX

SO Sequence 120 AA;

Query Match 100.0%; Score 26; DB 21; Length 120;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVDY 5
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DB 26 kvdyv 30

RESULT 12

ID AAG23318 standard; Protein; 126 AA.
XX AAG23318;
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XX 17-OCT-2000 (first entry)
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XX Arabidopsis thaliana protein fragment SEQ ID NO: 26582.
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XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 26582.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX

OS Arabidopsis thaliana.

XX
XX EPI033405-A2.
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PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

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XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
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RESULT 13

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DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 29810.

KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.

OS Arabidopsis thaliana.

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Query Match 100.0%; Score 26; DB 21; Length 129;
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DF 17-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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OS Arabidopsis thaliana.
XX
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XX
DT 17-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
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XX
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PR 01-SEP-1999; 99US-0151930.
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PR 13-SEP-1999; 99US-0153758.
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PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
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PR 12-OCT-1999; 99US-0158369.
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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
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PR 29-OCT-1999; 99US-0162142.

Query Match 100.0%; Score 26; DB 21; Length 135;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 29 kyydv 33

Search completed: August 9, 2001, 20:24:15
Job time: 249 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 9, 2001, 20:25:06 ; Search time 45.84 Seconds
(without alignments)
2.246 Million cell updates/sec

Title: US-09-367-013b-2_COPY_39_43
Perfect score: 26
Sequence: 1 KRYDV 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	26	100.0	254	3	US-08-906-616-129
3	26	100.0	254	4	US-08-639-075A-129
4	26	100.0	254	4	US-09-012-431-129
5	26	100.0	254	4	US-09-012-692-129
6	26	100.0	254	4	US-08-906-613-129
7	26	100.0	410	1	US-08-579-667-6
8	26	100.0	457	2	US-08-834-655-2
9	26	100.0	457	3	US-08-833-610-4
10	26	100.0	457	3	US-08-834-033A-2
11	26	100.0	457	4	US-08-334-033A-14
12	26	100.0	457	4	US-09-363-574-2
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15	25	96.2	156	2	US-09-098-900-4
16	25	96.2	156	3	US-08-806-877-4
17	25	96.2	177	3	US-08-764-563-3
18	25	96.2	263	1	US-07-901-707-4
19	25	96.2	263	1	US-07-988-430-4
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25	25	96.2	263	4	US-09-136-389-4
26	25	96.2	263	5	PCT-US92-09487-4
27	25	96.2	272	2	US-08-775-009-31

28	25	96.2	273	2	US-08-775-009-30	Sequence 30, Appl
29	25	96.2	286	1	US-08-324-301-13	Sequence 13, Appl
30	25	96.2	305	3	US-08-965-600-1	Sequence 1, Appl1
31	25	96.2	415	2	US-08-896-345-4	Sequence 4, Appl1
32	25	96.2	415	4	US-09-226-091-4	Sequence 4, Appl1
33	25	96.2	415	4	US-09-325-881-4	Sequence 4, Appl1
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37	24	92.3	157	4	US-08-328-322-15	Sequence 15, Appl
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39	24	92.3	298	2	US-08-838-543-5	Sequence 5, Appl1
40	23	88.5	79	3	US-08-993-254-3	Sequence 3, Appl1
41	23	88.5	93	3	US-08-946-329A-95	Sequence 95, Appl
42	23	88.5	95	3	US-08-946-329A-86	Sequence 86, Appl
43	23	88.5	96	3	US-08-946-329A-80	Sequence 80, Appl
44	23	88.5	134	2	US-08-801-972-4	Sequence 4, Appl1
45	23	88.5	134	3	US-09-178-881-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-08-906-769-129
; Sequence 129, Application US/08906769
; Patent No. 6077687
; GENERAL INFORMATION:
; APPLICANT: Grieve, Robert B.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wu Hunter, Shirley
; APPLICANT: Frank, Glenn R.
; APPLICANT: Stiegler, Gary
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Silver, Gary
; TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
; TITLE OF INVENTION: MOLECULES AND USES THEREOF
; NUMBER OF SEQUENCES: 190
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,769
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/639,075
; FILING DATE: 24-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-25-C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 129:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-906-769-129

Query Match 100.0%; Score 26; DB 3; Length 254;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYYDV 5
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DB 88 KYYDV 92

RESULT 2
US-08-906-616-129

; Sequence 129, Application US/08906616
; Patent No. 6121035

; GENERAL INFORMATION:

; APPLICANT: Griewe, Robert B.

; APPLICANT: Rushlow, Keith E.

; APPLICANT: Wu Hunter, Shirley

; APPLICANT: Stiegler, Gary

; APPLICANT: Gaines, Patrick J.

; APPLICANT: Silver, Gary

; TITLE OF INVENTION: FLEA AMINOPEPTIDASE PROTEINS AND USES THEREOF

; NUMBER OF SEQUENCES: 190

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sheridan Ross P.C.

; STREET: 1700 Lincoln Street, Suite 3500

; CITY: Denver

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80203

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/906,616

; FILING DATE: 05-AUG-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Connell, Gary J.

; REGISTRATION NUMBER: 32,020

; REFERENCE/DOCKET NUMBER: 2618-25-C2-3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (303) 863-9700

; TELEFAX: (303) 863-0223

; INFORMATION FOR SEQ ID NO: 129:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 254 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-906-616-129

QY 1 KYYDV 5
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DB 88 KYYDV 92

US-08-906-616-129

; Sequence 129, Application US/08639075A

; Patent No. 6150125

; GENERAL INFORMATION:

; APPLICANT: Griewe, Robert B.

; APPLICANT: Rushlow, Keith E.

; APPLICANT: Wu Hunter, Shirley

; APPLICANT: Frank, Glenn R.

; APPLICANT: Frank, Glenn R.

; APPLICANT: Stiegler, Gary
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Silver, Gary
; TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
; TITLE OF INVENTION: MOLECULES AND USES THEREOF
; NUMBER OF SEQUENCES: 190
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80203

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/639,075A

; FILING DATE: 24-APR-1996

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Connell, Gary J.

; REGISTRATION NUMBER: 32,020

; REFERENCE/DOCKET NUMBER: 2618-25-C2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (303) 863-9700

; TELEFAX: (303) 863-0223

; INFORMATION FOR SEQ ID NO: 129:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 254 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-639-075A-129

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DB 88 KYYDV 92

US-09-012-431-129

; Sequence 129, Application US/09012431

; Patent No. 6180383

; GENERAL INFORMATION:

; APPLICANT: Griewe, Robert B.

; APPLICANT: Rushlow, Keith E.

; APPLICANT: Wu Hunter, Shirley

; APPLICANT: Stiegler, Gary

; APPLICANT: Gaines, Patrick J.

; APPLICANT: Silver, Gary

; TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID

; TITLE OF INVENTION: MOLECULES AND USES THEREOF

; NUMBER OF SEQUENCES: 190

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sheridan Ross & McIntosh

; STREET: 1700 Lincoln Street, Suite 3500

; CITY: Denver

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80203

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; OPERATING SYSTEM: PC-DOS/MS-DOS

; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012.431
FILING DATE: 23-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 129:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 129:
US-09-012-431-129

Query Match 100.0%; Score 26; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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11111
DB 88 KVDV 92

RESULT 5
US-09-012-692-129
Sequence 129, Application US/09012692
Patent No. 6214579
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
APPLICANT: Silver, Gary
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,692
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 129:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-012-692-129

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Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDV 5
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DB 88 KVDV 92

RESULT 6
US-08-906-613-129
Sequence 129, Application US/08906613
Patent No. 6232096
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
APPLICANT: Silver, Gary
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,613
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 129:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-906-613-129

Query Match 100.0%; Score 26; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKYDV 5
11111
DB 88 KKYDV 92

RESULT 7

US-08-579-667-6
Sequence 6, Application US/08579667
Patent No. 5705624
GENERAL INFORMATION:
APPLICANT: Filizmaurice, Wayne P.
APPLICANT: Hellmann, Gary M.
APPLICANT: Grill, Laurence K.
APPLICANT: Kumagai, Monto H.
APPLICANT: Della-Cioppa, Guy R.
TITLE OF INVENTION: DNA SEQUENCES ENCODING ENZYMES USEFUL IN
PHYTOENE BIOSYNTHESIS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Virginia C. Bennett
STREET: 1211 East Morehead Street, PO Drawer 34009
CITY: Charlotte
STATE: No. 5705624th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,667
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 627-196
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-579-667-6

Query Match 100.0%; Score 26; DB 1; Length 410;

Best Local Similarity 100.0%; Pred. No. 99;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKYDV 5
11111
DB 78 KKYDV 82

RESULT 8

US-08-834-655-2
Sequence 2, Application US/08834655
Patent No. 5968809
GENERAL INFORMATION:
APPLICANT: KNUZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.124.0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-655-2

Query Match 100.0%; Score 26; DB 2; Length 457;

Best Local Similarity 100.0%; Pred. No. 1,1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKYDV 5
11111
DB 39 KKYDV 43

RESULT 9

US-08-833-610-4
Sequence 4, Application US/08833610
Patent No. 5972654
GENERAL INFORMATION:
APPLICANT: KNUZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,610
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.123.000US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)328-4400
TELEFAX: (650)328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-610-4

Query Match 100.0%; Score 26; DB 2; Length 457;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDV 5
|||||
Db 39 KVDV 43

RESULT 10
US-08-834-033A-2
Sequence 2, Application US/08834033A
Patent No. 6075183
GENERAL INFORMATION:
APPLICANT: KNOTZON, DEBORAH
APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,033A
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300,USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-033A-2

Query Match 100.0%; Score 26; DB 3; Length 457;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDV 5
|||||
Db 39 KVDV 43

RESULT 11
US-08-834-033A-14
Sequence 14, Application US/08834033A
Patent No. 6075183
GENERAL INFORMATION:
APPLICANT: KNOTZON, DEBORAH
APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,033A
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300,USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-033A-14

Query Match 100.0%; Score 26; DB 3; Length 457;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDV 5
|||||
Db 39 KVDV 43

RESULT 12
US-09-363-574-2
Sequence 2, Application US/09363574
Patent No. 6136574
GENERAL INFORMATION:
APPLICANT: KNOTZON, DEBORAH
APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG

APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,574
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-202 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-363-574-2

Query Match 100.0%; Score 26; DB 4; Length 457;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYYDV 5
Db 39 KYYDV 43

RESULT 13
US-07-749-541A-5
Sequence 5, Application US/07749541A
Patent No. 5317009
GENERAL INFORMATION:
APPLICANT: Lee-Huang, Sylvia
APPLICANT: Kung, Hsiang-fu
APPLICANT: Huang, Paul L.
APPLICANT: Huang, Philip L.
APPLICANT: Huang, Peter
APPLICANT: Huang, Henry I.
APPLICANT: Chen, Hao-chia
TITLE OF INVENTION: ANTI-HIV PROTEINS, GAP 31, DAP 30 AND DAP 32,
TITLE OF INVENTION: DNA CODING THEREFOR AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/749,541A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Litvack, Shmuel
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: LEE-HUANG-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)628-5197
TELEFAX: (202)737-3528
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: MAP 30
US-07-749-541A-5

Query Match 96.2%; Score 25; DB 1; Length 44;
Best Local Similarity 80.0%; Pred. No. 16;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYYDV 5
Db 30 KYYDI 34

RESULT 14
US-08-277-283-1
Sequence 1, Application US/08277283
Patent No. 548489
GENERAL INFORMATION:
APPLICANT: Lee-Huang, Sylvia
APPLICANT: Huang, Philip L.
APPLICANT: Nara, Peter L.
APPLICANT: Chen, Hao-chia
APPLICANT: Kung, Hsiang-fu
APPLICANT: Huang, Peter
APPLICANT: Huang, Henry I.
APPLICANT: Huang, Paul L.
TITLE OF INVENTION: A Plant Protein Useful for Treating Tumors
TITLE OF INVENTION: and HIV Infection
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/277,283
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/594,156
FILING DATE: 10/09/90
APPLICATION NUMBER: US 08/048,066
FILING DATE: 19-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Litvack, Shmuel

REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: LEE-HUANG-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)628-5197
TELEFAX: (202)727-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-277-283-1

Query Match 96.2%; Score 25; DB 1; Length 44;
Best Local Similarity 80.0%; Pred. NO. 16;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDV 5
||||:
Db 30 KVDI 34

RESULT 15
US-09-098-900-4
Sequence 4, Application US/09098900
Patent No. 5919629
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN CLATHRIN-ASSOCIATED
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,900
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/806,877
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0219 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-4166
TELEFAX: 415-855-0555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 406602
US-09-098-900-4

Query Match 96.2%; Score 25; DB 2; Length 156;

Best Local Similarity 80.0%; Pred. No. 62;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDV 5
||||:
Db 112 KVDI 116

Search completed: August 9, 2001, 20:25:06
Job time: 205 sec

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